



SEQUENCE LISTING

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GENERAL INFORMATION:

- I3
- (i) APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
 - (ii) TITLE OF INVENTION: Telomerase Reverse Transcriptase
 - (iii) NUMBER OF SEQUENCES: 479
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Townsend and Townsend and Crew LLP
 - (B) STREET: Two Embarcadero Center, Eighth Floor
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94111-3834
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/974,584
 - (B) FILING DATE: 19-NOV-1997
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/724,643
 - (B) FILING DATE: 01-OCT-1996
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/844,419
 - (B) FILING DATE: 18-APR-1997
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/846,017
 - (B) FILING DATE: 25-APR-1997
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/851,843
 - (B) FILING DATE: 06-MAY-1997
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/854,050
 - (B) FILING DATE: 09-MAY-1997
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/911,312
 - (B) FILING DATE: 14-AUG-1997

- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/912,951
 - (B) FILING DATE: 14-AUG-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/915,503
 - (B) FILING DATE: 14-AUG-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: WO PCT/US97/17618
 - (B) FILING DATE: 01-OCT-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: WO PCT/US97/17885
 - (B) FILING DATE: 01-OCT-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Einhorn, Gregory P.
 - (B) REGISTRATION NUMBER: 38,440
 - (C) REFERENCE/DOCKET NUMBER: 015389-002950US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 576-0200
 - (B) TELEFAX: (415) 576-0300

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 101..3196
 - (D) OTHER INFORMATION: /codon= (seq: "tga", aa: Cys)
/note= "Euplotes aediculatus 123 kD
telomerase subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT AACCTCAGTA	60
TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA ATG GAG GTT GAT GTT	115
Met Glu Val Asp Val	
1 5	
GAT AAT CAA GCT GAT AAT CAT GGC ATT CAC TCA GCT CTT AAG ACT TGT	163
Asp Asn Gln Ala Asp Asn His Gly Ile His Ser Ala Leu Lys Thr Cys	
10 15 20	
GAA GAA ATT AAA GAA GCT AAA ACG TTG TAC TCT TGG ATC CAG AAA GTT	211
Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser Trp Ile Gln Lys Val	
25 30 35	

ATT AGA TGA AGA AAT CAA TCT CAA AGT CAT TAT AAA GAT TTA GAA GAT	259
Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr Lys Asp Leu Glu Asp	
40 45 50	
ATT AAA ATA TTT GCG CAG ACA AAT ATT GTT GCT ACT CCA CGA GAC TAT	307
Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala Thr Pro Arg Asp Tyr	
55 60 65	
AAT GAA GAA GAT TTT AAA GTT ATT GCA AGA AAA GAA GTA TTT TCA ACT	355
Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys Glu Val Phe Ser Thr	
70 75 80 85	
GGA CTA ATG ATC GAA CTT ATT GAC AAA TGC TTA GTT GAA CTT CTT TCA	403
Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu Val Glu Leu Leu Ser	
90 95 100	
TCA AGC GAT GTT TCA GAT AGA CAA AAA CTT CAA TGA TTT GGA TTT CAA	451
Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln Cys Phe Gly Phe Gln	
105 110 115	
CTT AAG GGA AAT CAA TTA GCA AAG ACC CAT TTA TTA ACA GCT CTT TCA	499
Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu Leu Thr Ala Leu Ser	
120 125 130	
ACT CAA AAG CAG TAT TTC TTT CAA GAC GAA TGG AAC CAA GTT AGA GCA	547
Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp Asn Gln Val Arg Ala	
135 140 145	
ATG ATT GGA AAT GAG CTC TTC CGA CAT CTC TAC ACT AAA TAT TTA ATA	595
Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr Thr Lys Tyr Leu Ile	
150 155 160 165	
TTC CAG CGA ACT TCT GAA GGA ACT CTT GTT CAA TTT TGC GGG AAT AAC	643
Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln Phe Cys Gly Asn Asn	
170 175 180	
GTT TTT GAT CAT TTG AAA GTC AAC GAT AAG TTT GAC AAA AAG CAA AAA	691
Val Phe Asp His Leu Lys Val Asn Asp Lys Phe Asp Lys Lys Gln Lys	
185 190 195	
GGT GGA GCA GCA GAC ATG AAT GAA CCT CGA TGT TGA TCA ACC TGC AAA	739
Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys Cys Ser Thr Cys Lys	
200 205 210	
TAC AAT GTC AAG AAT GAG AAA GAT CAC TTT CTC AAC AAC ATC AAC GTG	787
Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu Asn Asn Ile Asn Val	
215 220 225	
CCG AAT TGG AAT AAT ATG AAA TCA AGA ACC AGA ATA TTT TAT TGC ACT	835
Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg Ile Phe Tyr Cys Thr	
230 235 240 245	
CAT TTT AAT AGA AAT AAC CAA TTC TTC AAA AAG CAT GAG TTT GTG AGT	883
His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys His Glu Phe Val Ser	
250 255 260	
AAC AAA AAC AAT ATT TCA GCG ATG GAC AGA GCT CAG ACG ATA TTC ACG	931
Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala Gln Thr Ile Phe Thr	
265 270 275	

AAT ATA TTC AGA TTT AAT AGA ATT AGA AAG AAG CTA AAA GAT AAG GTT Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys Leu Lys Asp Lys Val 280 285 290	979
ATC GAA AAA ATT GCC TAC ATG CTT GAG AAA GTC AAA GAT TTT AAC TTC Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val Lys Asp Phe Asn Phe 295 300 305	1027
AAC TAC TAT TTA ACA AAA TCT TGT CCT CTT CCA GAA AAT TGG CGG GAA Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro Glu Asn Trp Arg Glu 310 315 320 325	1075
CGG AAA CAA AAA ATC GAA AAC TTG ATA AAT AAA ACT AGA GAA GAA AAG Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys Thr Arg Glu Glu Lys 330 335 340	1123
TCG AAG TAC TAT GAA GAG CTG TTT AGC TAC ACA ACT GAT AAT AAA TGC Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr Thr Asp Asn Lys Cys 345 350 355	1171
GTC ACA CAA TTT ATT AAT GAA TTT TTC TAC AAT ATA CTC CCC AAA GAC Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn Ile Leu Pro Lys Asp 360 365 370	1219
TTT TTG ACT GGA AGA AAC CGT AAG AAT TTT CAA AAG AAA GTT AAG AAA Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln Lys Lys Val Lys Lys 375 380 385	1267
TAT GTG GAA CTA AAC AAG CAT GAA CTC ATT CAC AAA AAC TTA TTG CTT Tyr Val Glu Leu Asn Lys His Glu Leu Ile His Lys Asn Leu Leu Leu 390 395 400 405	1315
GAG AAG ATC AAT ACA AGA GAA ATA TCA TGG ATG CAG GTT GAG ACC TCT Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met Gln Val Glu Thr Ser 410 415 420	1363
GCA AAG CAT TTT TAT TAT TTT GAT CAC GAA AAC ATC TAC GTC TTA TGG Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn Ile Tyr Val Leu Trp 425 430 435	1411
AAA TTG CTC CGA TGG ATA TTC GAG GAT CTC GTC GTC TCG CTG ATT AGA Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg 440 445 450	1459
TGA TTT TTC TAT GTC ACC GAG CAA CAG AAA AGT TAC TCC AAA ACC TAT Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr 455 460 465	1507
TAC TAC AGA AAG AAT ATT TGG GAC GTC ATT ATG AAA ATG TCA ATC GCA Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala 470 475 480 485	1555
GAC TTA AAG AAG GAA ACG CTT GCT GAG GTC CAA GAA AAA GAG GTT GAA Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu 490 495 500	1603
GAA TGG AAA AAG TCG CTT GGA TTT GCA CCT GGA AAA CTC AGA CTA ATA Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile 505 510 515	1651

CCG AAG AAA ACT ACT TTC CGT CCA ATT ATG ACT TTC AAT AAG AAG ATT	1699
Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile	
520 525 530	
GTA AAT TCA GAC CGG AAG ACT ACA AAA TTA ACT ACA AAT ACG AAG TTA	1747
Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu	
535 540 545	
TTG AAC TCT CAC TTA ATG CTT AAG ACA TTG AAG AAT AGA ATG TTT AAA	1795
Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys	
550 555 560 565	
GAT CCT TTT GGA TTC GCT GTT TTT AAC TAT GAT GAT GTA ATG AAA AAG	1843
Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys	
570 575 580	
TAT GAG GAG TTT GTT TGC AAA TGG AAG CAA GTT GGA CAA CCA AAA CTC	1891
Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu	
585 590 595	
TTC TTT GCA ACT ATG GAT ATC GAA AAG TGA TAT GAT AGT GTA AAC AGA	1939
Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser Val Asn Arg	
600 605 610	
GAA AAA CTA TCA ACA TTC CTA AAA ACT ACT AAA TTA CTT TCT TCA GAT	1987
Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys Leu Leu Ser Ser Asp	
615 620 625	
TTC TGG ATT ATG ACT GCA CAA ATT CTA AAG AGA AAG AAT AAC ATA GTT	2035
Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg Lys Asn Asn Ile Val	
630 635 640 645	
ATC GAT TCG AAA AAC TTT AGA AAG AAA GAA ATG AAA GAT TAT TTT AGA	2083
Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met Lys Asp Tyr Phe Arg	
650 655 660	
CAG AAA TTC CAG AAG ATT GCA CTT GAA GGA GGA CAA TAT CCA ACC TTA	2131
Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly Gln Tyr Pro Thr Leu	
665 670 675	
TTC AGT GTT CTT GAA AAT GAA CAA AAT GAC TTA AAT GCA AAG AAA ACA	2179
Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu Asn Ala Lys Lys Thr	
680 685 690	
TTA ATT GTT GAA GCA AAG CAA AGA AAT TAT TTT AAG AAA GAT AAC TTA	2227
Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe Lys Lys Asp Asn Leu	
695 700 705	
CTT CAA CCA GTC ATT AAT ATT TGC CAA TAT AAT TAC ATT AAC TTT AAT	2275
Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn Tyr Ile Asn Phe Asn	
710 715 720 725	
GGG AAG TTT TAT AAA CAA ACA AAA GGA ATT CCT CAA GGT CTT TGA GTT	2323
Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val	
730 735 740	
TCA TCA ATT TTG TCA TCA TTT TAT TAT GCA ACA TTA GAG GAA AGC TCC	2371
Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser	
745 750 755	

TTA GGA TTC CTT AGA GAT GAA TCA ATG AAC CCT GAA AAT CCA AAT GTT Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn Pro Asn Val 760 765 770	2419
AAT CTT CTA ATG AGA CTT ACA GAT GAC TAT CTT TTG ATT ACA ACT CAA Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln 775 780 785	2467
GAG AAT AAT GCA GTA TTT TTT ATT GAG AAA CTT ATA AAC GTA AGT CGT Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg 790 795 800 805	2515
GAA AAT GGA TTT AAA TTC AAT ATG AAG AAA CTA CAG ACT AGT TTT CCA Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Ser Phe Pro 810 815 820	2563
TTA AGT CCA AGC AAA TTT GCA AAA TAC GGA ATG GAT AGT GTT GAG GAG Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met Asp Ser Val Glu Glu 825 830 835	2611
CAA AAT ATT GTT CAA GAT TAC TGC GAT TGG ATT GGC ATC TCA ATT GAT Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile Gly Ile Ser Ile Asp 840 845 850	2659
ATG AAA ACT CTT GCT TTA ATG CCA AAT ATT AAC TTG AGA ATA GAA GGA Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn Leu Arg Ile Glu Gly 855 860 865	2707
ATT CTG TGT ACA CTC AAT CTA AAC ATG CAA ACA AAG AAA GCA TCA ATG Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr Lys Lys Ala Ser Met 870 875 880 885	2755
TGG CTC AAG AAG AAA CTA AAG TCG TTT TTA ATG AAT AAC ATT ACC CAT Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met Asn Asn Ile Thr His 890 895 900	2803
TAT TTT AGA AAG ACG ATT ACA ACC GAA GAC TTT GCG AAT AAA ACT CTC Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe Ala Asn Lys Thr Leu 905 910 915	2851
AAC AAG TTA TTT ATA TCA GGC GGT TAC AAA TAC ATG CAA TGA GCC AAA Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Met Gln Cys Ala Lys 920 925 930	2899
GAA TAC AAG GAC CAC TTT AAG AAG AAC TTA GCT ATG AGC AGT ATG ATC Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala Met Ser Ser Met Ile 935 940 945	2947
GAC TTA GAG GTA TCT AAA ATT ATA TAC TCT GTA ACC AGA GCA TTC TTT Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Thr Arg Ala Phe Phe 950 955 960 965	2995
AAA TAC CTT GTG TGC AAT ATT AAG GAT ACA ATT TTT GGA GAG GAG CAT Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile Phe Gly Glu Glu His 970 975 980	3043
TAT CCA GAC TTT TTC CTT AGC ACA CTG AAG CAC TTT ATT GAA ATA TTC Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His Phe Ile Glu Ile Phe 985 990 995	3091

AGC ACA AAA AAG TAC ATT TTC AAC AGA GTT TGC ATG ATC CTC AAG GCA 3139
 Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys Met Ile Leu Lys Ala
 1000 1005 1010

AAA GAA GCA AAG CTA AAA AGT GAC CAA TGT CAA TCT CTA ATT CAA TAT 3187
 Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln Ser Leu Ile Gln Tyr
 1015 1020 1025

GAT GCA TAGTCGACTA TTCTAACTTA TTTTGGAAAG TTAATTTTCA ATTTTGTCT 3243
 Asp Ala
 1030

TATATACTGG GGTTTTGGGG TTTTGGGGTT TTGGGG 3279

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser
 1 5 10 15

Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser
 20 25 30

Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
 35 40 45

Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala
 50 55 60

Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys
 65 70 75 80

Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu
 85 90 95

Val Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln
 100 105 110

Cys Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu
 115 120 125

Leu Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp
 130 135 140

Asn Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr
 145 150 155 160

Thr Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln
 165 170 175

Phe Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe
 180 185 190

Asp Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys
 195 200 205
 Cys Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu
 210 215 220
 Asn Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg
 225 230 235 240
 Ile Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys
 245 250 255
 His Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala
 260 265 270
 Gln Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys
 275 280 285
 Leu Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val
 290 295 300
 Lys Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro
 305 310 315 320
 Glu Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys
 325 330 335
 Thr Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr
 340 345 350
 Thr Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn
 355 360 365
 Ile Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln
 370 375 380
 Lys Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His
 385 390 395 400
 Lys Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met
 405 410 415
 Gln Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn
 420 425 430
 Ile Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val
 435 440 445
 Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser
 450 455 460
 Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met
 465 470 475 480
 Lys Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln
 485 490 495
 Glu Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly
 500 505 510

Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr
 515 520 525
 Phe Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr
 530 535 540
 Thr Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys
 545 550 555 560
 Asn Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp
 565 570 575
 Asp Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val
 580 585 590
 Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
 595 600 605
 Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
 610 615 620
 Leu Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg
 625 630 635 640
 Lys Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met
 645 650 655
 Lys Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly
 660 665 670
 Gln Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu
 675 680 685
 Asn Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe
 690 695 700
 Lys Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn
 705 710 715 720
 Tyr Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro
 725 730 735
 Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr
 740 745 750
 Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro
 755 760 765
 Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu
 770 775 780
 Leu Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu
 785 790 795 800
 Ile Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu
 805 810 815
 Gln Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met
 820 825 830

Asp Ser Val Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile;
 835 840 845
 Gly Ile Ser Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn
 850 855 860
 Leu Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr
 865 870 875 880
 Lys Lys Ala Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met
 885 890 895
 Asn Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe
 900 905 910
 Ala Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr
 915 920 925
 Met Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala
 930 935 940
 Met Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val
 945 950 955 960
 Thr Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile
 965 970 975
 Phe Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His
 980 985 990
 Phe Ile Glu Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys
 995 1000 1005
 Met Ile Leu Lys Ala Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln
 1010 1015 1020
 Ser Leu Ile Gln Tyr Asp Ala
 1025 1030

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1762
- (D) OTHER INFORMATION: /note= "DNA encoding three open reading frames (ORF) for Euplotes aediculatus 43 kD telomerase protein subunit given in SEQ ID NOS:4-6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCCAAAACC CCAAAACCCC AAAACCCCTA TAAAAAAGA AAAAATTGAG GTAGTTTAGA	60
AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA TTTGGATGAT ATAGAAAATT	120
TACTTCCTAA TACATTCAAC AAGTATAGCA GCTCTTGTAG TGACAAGAAA GGATGCAAAA	180
CATTGAAATC TGGCTCGAAA TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG	240
AGTTCTACTT CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA	300
AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA AATCAGGTAA	360
TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA TTATGGAGAA AATTACTTAA	420
TACTAAAAGG TAAACAGTTT GGATTATTTT CCTAGCCAAC AATGATGAGT ATATTAAATT	480
CATATGAGAA TGAGTCAAAG GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT	540
AAAACGCAAG AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTTCG	600
TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC TTGAGACAAT	660
TGAAAAAGCT GTTTACAACG GAAGGAATCG CAGTTCTGAA AGTTCTGATG TGTATGCCAT	720
TATTTTGTGA ATTAATCTCA AATATCTTAT CTCAATTTAA TGGATAGCTA TAGAAACAAA	780
CCAAATAAAC CATGCAAGTT TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC	840
TGAATTTATA TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC	900
TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT AAAAGAAGCA	960
GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT TTGTTGATTC TTCTGTAACC	1020
GGAATTAACA ACAAGAATAT TAGCAACGAA AAAGAAGAAG AGCTATCACA ATCCTGATTC	1080
TTAAAGATTT CAAAAATTCC AGGTAAGAGA GATACATTCA TTAATTTCA TATATTATAG	1140
TTTTTCATTT CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA	1200
GTA AAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT TCACATTCAT	1260
AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA GCAGTCATCC GTTTTAAAAA	1320
TAGTGCTATG AGGACTAAAT TTTTAGAGTC AAGAAATGGA GCCGAAATCT TAATCAAAAA	1380
GAATTGCGTC GATATTGCAA AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA	1440
ATCTTGATTG ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATTA AAGAAATAAA	1500
GTA ACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG CGATCTTCAA	1560
TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA ATACAAACCT TGGTCAAAAT	1620
ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA AAAGAAAAAA TAAGGCAATA AATAAAATGA	1680
GTACAGAAGT GAAGAAATAA AAGATTTATT TTTTCAATA ATTTATTGAA AAGAGGGGTT	1740
TTGGGGTTTT GGGGTTTTGG GG	1762

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..300
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 1-300 may be
present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 630
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at position 630 may be
present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 649..663
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 649-663 may be
present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 674..688
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 674-688 may be
present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 701..706
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 701-706 may be
present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 771..790
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 771-790 may be
present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 887..937
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 887-937 may be
present or absent"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 965..994
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa at positions 965-994 may be
 present or absent"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 1018..1027
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa at positions 1018-1027 may
 be present or absent"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	1	5	10	15
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	20	25	30	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	35	40	45	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	50	55	60	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	65	70	75	80
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	85	90	95	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	100	105	110	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	115	120	125	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	130	135	140	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	145	150	155	160
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	165	170	175	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	180	185	190	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	195	200	205	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	210	215	220	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	225	230	235	240

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
245 250 255
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
260 265 270
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
275 280 285
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
290 295 300
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
305 310 315 320
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
325 330 335
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
340 345 350
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
355 360 365
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
370 375 380
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
385 390 395 400
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
405 410 415
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
420 425 430
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
435 440 445
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
450 455 460
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
465 470 475 480
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
485 490 495
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
500 505 510
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
515 520 525
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
530 535 540
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
545 550 555 560

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
565 570 575
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
580 585 590
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
595 600 605
Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa
610 615 620
Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa
625 630 635 640
Xaa Xaa Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
645 650 655
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Val Xaa Xaa Xaa Xaa Xaa
660 665 670
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
675 680 685
Xaa Xaa Xaa Arg Xaa Xaa Pro Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
690 695 700
Xaa Xaa Arg Xaa Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
705 710 715 720
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
725 730 735
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
740 745 750
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
755 760 765
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
770 775 780
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Asp Xaa
785 790 795 800
Xaa Xaa Xaa Tyr Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
805 810 815
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
820 825 830
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
835 840 845
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
850 855 860
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
865 870 875 880

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 885 890 895
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 900 905 910
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 915 920 925
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Gly Xaa
 930 935 940
 Xaa Gln Gly Xaa Xaa Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 945 950 955 960
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 965 970 975
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 980 985 990
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Asp Xaa Leu Xaa Xaa Xaa Xaa
 995 1000 1005
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1010 1015 1020
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys
 1025 1030 1035 1040

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCCGGATCC TGCGCATGTG TGAGCCGAGT CCTGGG

36

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Val Asp Asp Phe Leu
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Trp Xaa Gly Xaa Ser Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 6
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Xaa Leu Gly Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 83 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp	Ile	Asp	Leu	Asp	Asp	Ile	Glu	Asn	Leu	Leu	Pro	Asn	Thr	Phe	Asn	
1				5					10					15		
Lys	Tyr	Ser	Ser	Ser	Cys	Ser	Asp	Lys	Lys	Gly	Cys	Lys	Thr	Leu	Lys	
			20					25					30			
Ser	Gly	Ser	Lys	Ser	Pro	Ser	Leu	Thr	Ile	Pro	Lys	Leu	Gln	Lys	Gln	
			35				40					45				
Leu	Glu	Phe	Tyr	Phe	Ser	Asp	Ala	Asn	Leu	Tyr	Asn	Asp	Ser	Phe	Leu	
	50					55					60					
Arg	Lys	Leu	Val	Leu	Lys	Ser	Gly	Glu	Gln	Arg	Val	Glu	Ile	Glu	Thr	
65					70					75				80		
Leu	Leu	Met														

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asn	Val	Lys	Ser	Ala	Lys	Ile	Glu	Ser	Ser	Ser	Leu	Glu	Ser	Leu	Glu	
1				5					10					15		
Asp	Ile	Asp	Ser	Leu	Cys	Lys	Ser	Ile	Ala	Ser	Cys	Lys	Asn	Leu	Gln	
			20					25					30			
Asn	Val	Asn	Ile	Ile	Ala	Ser	Leu	Leu	Tyr	Pro	Asn	Asn	Ile	Gln	Lys	
			35				40					45				
Asn	Pro	Phe	Asn	Lys	Pro	Asn	Leu	Leu	Phe	Phe	Lys	Gln	Phe	Glu	Gln	
	50					55					60					
Leu	Lys	Asn	Leu	Glu	Asn	Val	Ser	Ile	Asn	Cys	Ile	Leu	Asp	Gln	His	
65					70					75				80		
Ile	Leu	Asn	Ser	Ile	Ser	Glu	Phe	Leu	Glu	Lys	Asn	Lys	Lys	Ile	Lys	
				85					90					95		

Ala Phe Ile Leu
100

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Glu Met Asp Ile Asp Leu Asp Asp Ile Glu Asn Leu Leu Pro Asn
1 5 10 15
Thr Phe Asn Lys Tyr Ser Ser Ser Cys Ser Asp Lys Lys Gly Cys Lys
20 25 30
Thr Leu Lys Ser Gly Ser Lys Ser Pro Ser Leu Thr Ile Pro Lys Leu
35 40 45
Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn Asp
50 55 60
Ser Phe Leu Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val Glu
65 70 75 80
Ile Glu Thr Leu Leu
85

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ile Glu Leu Ala Ile Lys Ile Ala Val Asn Lys Asn Leu Asp Glu Ile
1 5 10 15
Lys Gly His Thr Ala Ile Phe Ser Asp Val Ser Gly Ser Met Ser Thr
20 25 30
Ser Met Ser Gly Gly Ala Lys Lys Tyr Gly Ser Val Arg Thr Cys Leu
35 40 45
Glu Cys Ala Leu Val Leu Gly Leu Met Val Lys Gln Arg Cys Glu Lys
50 55 60

Ser	Ser	Phe	Tyr	Ile	Phe	Ser	Ser	Pro	Ser	Ser	Gln	Cys	Asn	Lys	Cys
65					70				75						80
Tyr	Leu	Glu	Val	Asp	Leu	Pro	Gly	Asp	Glu	Leu	Arg	Pro	Ser	Met	Gln
				85					90					95	
Lys Leu Leu															

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 5
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Xaa	Xaa	Asp	Asp	Xaa
1				5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Val"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Phe or Tyr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Xaa Xaa Asp Asp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Phe or Tyr"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Xaa Xaa Asp Asp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Leu or Ile"

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7..8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10..11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 25
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = polar amino acid,
 selected from Gly, Ser, Thr, Tyr, Cys,
 Asn or Gln"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 28..29
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Phe or Tyr"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 31
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Phe	Tyr
1				5					10						15	
Xaa	Thr	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa	Xaa
			20					25						30		
Xaa	Trp															

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Leu or Ile"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 7..8
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 10..11
 (D) OTHER INFORMATION: /product= "OTHER"

/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

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(ix) FEATURE:
  (A) NAME/KEY: Modified-site
  (B) LOCATION: 12
  (D) OTHER INFORMATION: /product= "OTHER"
                        /note= "Xaa = Gln or Arg"

(ix) FEATURE:
  (A) NAME/KEY: Modified-site
  (B) LOCATION: 13
  (D) OTHER INFORMATION: /product= "OTHER"
                        /note= "Xaa = polar amino acid,
                        selected from Gly, Ser, Thr, Tyr, Cys,
                        Asn or Gln"

(ix) FEATURE:
  (A) NAME/KEY: Modified-site
  (B) LOCATION: 21
  (D) OTHER INFORMATION: /product= "OTHER"
                        /note= "Xaa = polar amino acid,
                        selected from Gly, Ser, Thr, Tyr, Cys,
                        Asn or Gln"

(ix) FEATURE:
  (A) NAME/KEY: Modified-site
  (B) LOCATION: 25
  (D) OTHER INFORMATION: /product= "OTHER"
                        /note= "Xaa = polar amino acid,
                        selected from Gly, Ser, Thr, Tyr, Cys,
                        Asn or Gln"

(ix) FEATURE:
  (A) NAME/KEY: Modified-site
  (B) LOCATION: 29..30
  (D) OTHER INFORMATION: /product= "OTHER"
                        /note= "Xaa = Phe or Tyr"

(ix) FEATURE:
  (A) NAME/KEY: Modified-site
  (B) LOCATION: 32
  (D) OTHER INFORMATION: /product= "OTHER"
                        /note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
1      5      10      15

Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa
20      25      30

Xaa Xaa Trp
35

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(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gly Ser Val Thr Lys
1 5

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Asn Ser Ala Val Asp
1 5

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTTCAAGACC ATCCTGGACT TTCGAAACGC GGCCGCCACC GCGGTGGAGC TCC

53

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Leu Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn
1 5 10 15
Asp Ser Phe Leu Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val
20 25 30
Glu Ile Glu Thr Leu Leu Met
35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Ile Cys His Gln Xaa Glu Tyr Tyr Phe Gly Asp Phe Asn Leu Pro Arg
1 5 10 15
Asp Lys Phe Leu Lys Glu Gln Ile Lys Leu Asp Glu Gly Trp Val Pro
20 25 30
Leu Glu Ile Met Ile Lys
35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Ile Cys Glu Gln Ile Glu Tyr Tyr Phe Gly Asp His Asn Leu Pro Arg
1 5 10 15
Asp Lys Phe Leu Lys Gln Gln Ile Leu Leu Asp Asp Gly Trp Val Pro
20 25 30
Leu Glu Thr Met Ile Lys
35

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ile	Leu	Arg	Gln	Val	Glu	Tyr	Tyr	Phe	Gly	Asp	Ala	Asn	Leu	Asn	Arg
1				5					10					15	
Asp	Lys	Phe	Leu	Arg	Glu	Gln	Ile	Gly	Lys	Asn	Glu	Asp	Gly	Trp	Val
			20					25					30		
Pro	Leu	Ser	Val	Leu	Val	Thr									
			35												

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Cys	Leu	Lys	Gln	Val	Glu	Phe	Tyr	Phe	Ser	Glu	Phe	Asn	Phe	Pro	Tyr
1				5					10					15	
Asp	Arg	Phe	Leu	Arg	Thr	Thr	Ala	Glu	Lys	Asn	Asp	Gly	Trp	Val	Pro
			20					25					30		
Ile	Ser	Thr	Ile	Ala	Thr										
			35												

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TAGACCTGTT AGTGACATT TGAATTGAAG C

31

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TAGACCTGTT AGGTTGGATT TGTGGCATCA

30

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAAAACCCCA AAACCTAACA GGTCTA

26

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCGGGAATTC TAATACGACT CACTATAGGG AAGAACTCT GATGAGGCCG AAAGGCCGAA

60

ACTCCACGAA AGTGGAGTAA GTTTCTCGAT AATTGATCTG TAG

103

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGGGGATCCT CTTCAAAGA TGAGAGGACA GCAAAC 36

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCCCAAAACC CCAAACCCC AAAACCCCA CAGGGGTTTT GGGGTTTGG GTTTTGGGG 60

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCAAAACCCC AAAACCCCAA AACCCCAACA GGGGTTTGG GTTTTGGGG TTTTGGGG 58

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAAACCCCAA AACCCAAAA CCCCACAGG GGTTTTGGGG TTTTGGGGTT TTGGGG 56

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AACCCCAAAA CCCCAAACC CCCACAGGGG TTTTGGGGTT TTGGGGTTTT GGGG 54

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CCCCAAAACC CCAAACCCC CACAGGGGTT TTGGGGTTTT GGGGTTTT 48

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AAAACCCCAA AACCCCAAAA CCCCACAGG GGTTTTGGGG TTTTGGGGTT TT 52

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AACCCCAAAA CCCCAAACC CCCACAGGGG TTTTGGGGTT TTGGGGTTTT 50

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GGGGAAGCTT TAATACGACT CACTATAGGG TTGCGGAGGG TGGGCCTG

48

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCAAAACCCC AAAACCCCCA CAGGGGTTTT GGGGTTTTGG GGTTTT

46

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAAACCCCCA AACCCCCACA GGGGTTTTGG GGTTTTGGGG TTTT

44

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:
CAAAACCCCA AAACC 15

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:
TTTTGGGG 8

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:
GGGGTTTT 8

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Arg Phe Ile Pro Lys Pro
1 5

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:
TCTRAARTAR TGDGTNADRT TRTTCAT 27

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:
GCGGATCCAT GAAAYCCWGAR AAYCCWAAYG T 31

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:
NNNGTNACHG GHATHAAYAA 20

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:
DGCDGTYTCY TGRTCRTTTRT A 21

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 92..2251
- (D) OTHER INFORMATION: /codon= (seq: "taa", aa: Gln)
/codon= (seq: "tag", aa: Gln)
/note= "Tetrahymena thermophila 80 kD
TRT protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AACTCATTTA ATTACTAATT TAATCAACAA GATTGATAAA AAGCAGTAAA TAAAACCCAA	60
TAGATTTAAT TTAGAAAGTA TCAATTGAAA A ATG GAA ATT GAA AAC AAC TAA	112
Met Glu Ile Glu Asn Asn Gln	
1 5	
GCA CAA TAG CCA AAA GCC GAA AAA TTG TGG TGG GAA CTT GAA TTA GAG	160
Ala Gln Gln Pro Lys Ala Glu Lys Leu Trp Trp Glu Leu Glu Leu Glu	
10 15 20	
ATG CAA GAA AAC CAA AAT GAT ATA TAA GTT AGG GTT AAG ATT GAC GAT	208
Met Gln Glu Asn Gln Asn Asp Ile Gln Val Arg Val Lys Ile Asp Asp	
25 30 35	
CCT AAG CAA TAT CTC GTG AAC GTC ACT GCA GCA TGT TTG TTG TAG GAA	256
Pro Lys Gln Tyr Leu Val Asn Val Thr Ala Ala Cys Leu Leu Gln Glu	
40 45 50 55	
GGT AGT TAC TAC TAA GAT AAA GAT GAA AGA AGA TAT ATC ATC ACT AAA	304
Gly Ser Tyr Tyr Gln Asp Lys Asp Glu Arg Arg Tyr Ile Ile Thr Lys	
60 65 70	
GCA CTT CTT GAG GTG GCT GAG TCT GAT CCT GAG TTC ATC TGC TAG TTG	352
Ala Leu Leu Glu Val Ala Glu Ser Asp Pro Glu Phe Ile Cys Gln Leu	
75 80 85	
GCA GTC TAC ATC CGT AAT GAA CTT TAC ATC AGA ACT ACC ACT AAC TAC	400
Ala Val Tyr Ile Arg Asn Glu Leu Tyr Ile Arg Thr Thr Thr Asn Tyr	
90 95 100	
ATT GTA GCA TTT TGT GTT GTC CAC AAG AAT ACT CAA CCA TTC ATC GAA	448
Ile Val Ala Phe Cys Val Val His Lys Asn Thr Gln Pro Phe Ile Glu	
105 110 115	
AAG TAC TTC AAC AAA GCA GTA CTT TTG CCT AAT GAC TTA CTG GAA GTC	496
Lys Tyr Phe Asn Lys Ala Val Leu Leu Pro Asn Asp Leu Leu Glu Val	
120 125 130 135	

TGT GAA TTT GCA TAG GTT CTC TAT ATT TTT GAT GCA ACT GAA TTC AAA	544
Cys Glu Phe Ala Gln Val Leu Tyr Ile Phe Asp Ala Thr Glu Phe Lys	
140 145 150	
AAT TTG TAT CTT GAT AGG ATA CTT TCA TAA GAT ATT CGT AAG GAA CTC	592
Asn Leu Tyr Leu Asp Arg Ile Leu Ser Gln Asp Ile Arg Lys Glu Leu	
155 160 165	
ACT TTC CGT AAG TGT TTA CAA AGA TGC GTC AGA AGC AAG TTT TCT GAA	640
Thr Phe Arg Lys Cys Leu Gln Arg Cys Val Arg Ser Lys Phe Ser Glu	
170 175 180	
TTG AAC GAA TAC TAA CTT GGT AAG TAT TGC ACT GAA TCC TAA CGT AAG	688
Phe Asn Glu Tyr Gln Leu Gly Lys Tyr Cys Thr Glu Ser Gln Arg Lys	
185 190 195	
AAA ACA ATG TTC CGT TAC CTC TCA GTT ACC AAC AAG TAA AAG TGG GAT	736
Lys Thr Met Phe Arg Tyr Leu Ser Val Thr Asn Lys Gln Lys Trp Asp	
200 205 210 215	
TAA ACT AAG AAG AAG AGA AAA GAG AAT CTC TTA ACC AAA CTT TAG GCA	784
Gln Thr Lys Lys Lys Arg Lys Glu Asn Leu Leu Thr Lys Leu Gln Ala	
220 225 230	
ATA AAG GAA TCT GAA GAT AAG TCC AAG AGA GAA ACT GGA GAC ATA ATG	832
Ile Lys Glu Ser Glu Asp Lys Ser Lys Arg Glu Thr Gly Asp Ile Met	
235 240 245	
AAC GTT GAA GAT GCA ATC AAG GCT TTA AAA CCA GCA GTT ATG AAG AAA	880
Asn Val Glu Asp Ala Ile Lys Ala Leu Lys Pro Ala Val Met Lys Lys	
250 255 260	
ATA GCC AAG AGA TAG AAT GCC ATG AAG AAA CAC ATG AAG GCA CCT AAA	928
Ile Ala Lys Arg Gln Asn Ala Met Lys Lys His Met Lys Ala Pro Lys	
265 270 275	
ATT CCT AAC TCT ACC TTG GAA TCA AAG TAC TTG ACC TTC AAG GAT CTC	976
Ile Pro Asn Ser Thr Leu Glu Ser Lys Tyr Leu Thr Phe Lys Asp Leu	
280 285 290 295	
ATT AAG TTC TGC CAT ATT TCT GAG CCT AAA GAA AGA GTC TAT AAG ATC	1024
Ile Lys Phe Cys His Ile Ser Glu Pro Lys Glu Arg Val Tyr Lys Ile	
300 305 310	
CTT GGT AAA AAA TAC CCT AAG ACC GAA GAG GAA TAC AAA GCA GCC TTT	1072
Leu Gly Lys Lys Tyr Pro Lys Thr Glu Glu Glu Tyr Lys Ala Ala Phe	
315 320 325	
GGT GAT TCT GCA TCT GCA CCC TTC AAT CCT GAA TTG GCT GGA AAG CGT	1120
Gly Asp Ser Ala Ser Ala Pro Phe Asn Pro Glu Leu Ala Gly Lys Arg	
330 335 340	
ATG AAG ATT GAA ATC TCT AAA ACA TGG GAA AAT GAA CTC AGT GCA AAA	1168
Met Lys Ile Glu Ile Ser Lys Thr Trp Glu Asn Glu Leu Ser Ala Lys	
345 350 355	
GGC AAC ACT GCT GAG GTT TGG GAT AAT TTA ATT TCA AGC AAT TAA CTC	1216
Gly Asn Thr Ala Glu Val Trp Asp Asn Leu Ile Ser Ser Asn Gln Leu	
360 365 370 375	

CCA TAT ATG GCC ATG TTA CGT AAC TTG TCT AAC ATC TTA AAA GCC GGT	1264
Pro Tyr Met Ala Met Leu Arg Asn Leu Ser Asn Ile Leu Lys Ala Gly	
380 385 390	
GTT TCA GAT ACT ACA CAC TCT ATT GTG ATC AAC AAG ATT TGT GAG CCC	1312
Val Ser Asp Thr Thr His Ser Ile Val Ile Asn Lys Ile Cys Glu Pro	
395 400 405	
AAG GCC GTT GAG AAC TCC AAG ATG TTC CCT CTT CAA TTC TTT AGT GCC	1360
Lys Ala Val Glu Asn Ser Lys Met Phe Pro Leu Gln Phe Phe Ser Ala	
410 415 420	
ATT GAA GCT GTT AAT GAA GCA GTT ACT AAG GGA TTC AAG GCC AAG AAG	1408
Ile Glu Ala Val Asn Glu Ala Val Thr Lys Gly Phe Lys Ala Lys Lys	
425 430 435	
AGA GAA AAT ATG AAT CTT AAA GGT CAA ATC GAA GCA GTA AAG GAA GTT	1456
Arg Glu Asn Met Asn Leu Lys Gly Gln Ile Glu Ala Val Lys Glu Val	
440 445 450 455	
GTT GAA AAA ACC GAT GAA GAG AAG AAA GAT ATG GAG TTG GAG TAA ACC	1504
Val Glu Lys Thr Asp Glu Glu Lys Lys Asp Met Glu Leu Glu Gln Thr	
460 465 470	
GAA GAA GGA GAA TTT GTT AAA GTC AAC GAA GGA ATT GGC AAG CAA TAC	1552
Glu Glu Gly Glu Phe Val Lys Val Asn Glu Gly Ile Gly Lys Gln Tyr	
475 480 485	
ATT AAC TCC ATT GAA CTT GCA ATC AAG ATA GCA GTT AAC AAG AAT TTA	1600
Ile Asn Ser Ile Glu Leu Ala Ile Lys Ile Ala Val Asn Lys Asn Leu	
490 495 500	
GAT GAA ATC AAA GGA CAC ACT GCA ATC TTC TCT GAT GTT TCT GGT TCT	1648
Asp Glu Ile Lys Gly His Thr Ala Ile Phe Ser Asp Val Ser Gly Ser	
505 510 515	
ATG AGT ACC TCA ATG TCA GGT GGA GCC AAG AAG TAT GGT TCC GTT CGT	1696
Met Ser Thr Ser Met Ser Gly Gly Ala Lys Lys Tyr Gly Ser Val Arg	
520 525 530 535	
ACT TGT CTC GAG TGT GCA TTA GTC CTT GGT TTG ATG GTA AAA TAA CGT	1744
Thr Cys Leu Glu Cys Ala Leu Val Leu Gly Leu Met Val Lys Gln Arg	
540 545 550	
TGT GAA AAG TCC TCA TTC TAC ATC TTC AGT TCA CCT AGT TCT CAA TGC	1792
Cys Glu Lys Ser Ser Phe Tyr Ile Phe Ser Ser Pro Ser Ser Gln Cys	
555 560 565	
AAT AAG TGT TAC TTA GAA GTT GAT CTC CCT GGA GAC GAA CTC CGT CCT	1840
Asn Lys Cys Tyr Leu Glu Val Asp Leu Pro Gly Asp Glu Leu Arg Pro	
570 575 580	
TCT ATG TAA AAA CTT TTG CAA GAG AAA GGA AAA CTT GGT GGT GGT ACT	1888
Ser Met Gln Lys Leu Leu Gln Glu Lys Gly Lys Leu Gly Gly Gly Thr	
585 590 595	
GAT TTC CCC TAT GAG TGC ATT GAT GAA TGG ACA AAG AAT AAA ACT CAC	1936
Asp Phe Pro Tyr Glu Cys Ile Asp Glu Trp Thr Lys Asn Lys Thr His	
600 605 610 615	

GTA GAC AAT ATC GTT ATT TTG TCT GAT ATG ATG ATT GCA GAA GGA TAT	1984
Val Asp Asn Ile Val Ile Leu Ser Asp Met Met Ile Ala Glu Gly Tyr	
620 625 630	
TCA GAT ATC AAT GTT AGA GGC AGT TCC ATT GTT AAC AGC ATC AAA AAG	2032
Ser Asp Ile Asn Val Arg Gly Ser Ser Ile Val Asn Ser Ile Lys Lys	
635 640 645	
TAC AAG GAT GAA GTA AAT CCT AAC ATT AAA ATC TTT GCA GTT GAC TTA	2080
Tyr Lys Asp Glu Val Asn Pro Asn Ile Lys Ile Phe Ala Val Asp Leu	
650 655 660	
GAA GGT TAC GGA AAG TGC CTT AAT CTA GGT GAT GAG TTC AAT GAA AAC	2128
Glu Gly Tyr Gly Lys Cys Leu Asn Leu Gly Asp Glu Phe Asn Glu Asn	
665 670 675	
AAC TAC ATC AAG ATA TTC GGT ATG AGC GAT TCA ATC TTA AAG TTC ATT	2176
Asn Tyr Ile Lys Ile Phe Gly Met Ser Asp Ser Ile Leu Lys Phe Ile	
680 685 690 695	
TCA GCC AAG CAA GGA GGA GCA AAT ATG GTC GAA GTT ATC AAA AAC TTT	2224
Ser Ala Lys Gln Gly Gly Ala Asn Met Val Glu Val Ile Lys Asn Phe	
700 705 710	
GCC CTT CAA AAA ATA GGA CAA AAG TGAGTTTCTT GAGATTCTTC TATAACAAAA	2278
Ala Leu Gln Lys Ile Gly Gln Lys	
715	
ATCTCACCCC ACTTTTTTGT TTTATTGCAT AGCCATTATG AAATTTAAAT TATTATCTAT	2338
TTATTTAAGT TACTTACATA GTTTATGTAT CGCAGTCTAT TAGCCTATTC AAATGATTCT	2398
GCAAAGAACA AAAAAAGATTA AAA	2421

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Glu Ile Glu Asn Asn Gln Ala Gln Gln Pro Lys Ala Glu Lys Leu
1 5 10 15
Trp Trp Glu Leu Glu Leu Glu Met Gln Glu Asn Gln Asn Asp Ile Gln
20 25 30
Val Arg Val Lys Ile Asp Asp Pro Lys Gln Tyr Leu Val Asn Val Thr
35 40 45
Ala Ala Cys Leu Leu Gln Glu Gly Ser Tyr Tyr Gln Asp Lys Asp Glu
50 55 60
Arg Arg Tyr Ile Ile Thr Lys Ala Leu Leu Glu Val Ala Glu Ser Asp
65 70 75 80

Pro	Glu	Phe	Ile	Cys	Gln	Leu	Ala	Val	Tyr	Ile	Arg	Asn	Glu	Leu	Tyr	
				85					90						95	
Ile	Arg	Thr	Thr	Thr	Asn	Tyr	Ile	Val	Ala	Phe	Cys	Val	Val	His	Lys	
			100					105					110			
Asn	Thr	Gln	Pro	Phe	Ile	Glu	Lys	Tyr	Phe	Asn	Lys	Ala	Val	Leu	Leu	
		115					120					125				
Pro	Asn	Asp	Leu	Leu	Glu	Val	Cys	Glu	Phe	Ala	Gln	Val	Leu	Tyr	Ile	
	130					135					140					
Phe	Asp	Ala	Thr	Glu	Phe	Lys	Asn	Leu	Tyr	Leu	Asp	Arg	Ile	Leu	Ser	
145					150					155					160	
Gln	Asp	Ile	Arg	Lys	Glu	Leu	Thr	Phe	Arg	Lys	Cys	Leu	Gln	Arg	Cys	
				165					170					175		
Val	Arg	Ser	Lys	Phe	Ser	Glu	Phe	Asn	Glu	Tyr	Gln	Leu	Gly	Lys	Tyr	
			180					185					190			
Cys	Thr	Glu	Ser	Gln	Arg	Lys	Lys	Thr	Met	Phe	Arg	Tyr	Leu	Ser	Val	
		195					200					205				
Thr	Asn	Lys	Gln	Lys	Trp	Asp	Gln	Thr	Lys	Lys	Lys	Arg	Lys	Glu	Asn	
	210					215						220				
Leu	Leu	Thr	Lys	Leu	Gln	Ala	Ile	Lys	Glu	Ser	Glu	Asp	Lys	Ser	Lys	
225					230					235					240	
Arg	Glu	Thr	Gly	Asp	Ile	Met	Asn	Val	Glu	Asp	Ala	Ile	Lys	Ala	Leu	
			245						250					255		
Lys	Pro	Ala	Val	Met	Lys	Lys	Ile	Ala	Lys	Arg	Gln	Asn	Ala	Met	Lys	
			260					265					270			
Lys	His	Met	Lys	Ala	Pro	Lys	Ile	Pro	Asn	Ser	Thr	Leu	Glu	Ser	Lys	
		275					280					285				
Tyr	Leu	Thr	Phe	Lys	Asp	Leu	Ile	Lys	Phe	Cys	His	Ile	Ser	Glu	Pro	
	290					295					300					
Lys	Glu	Arg	Val	Tyr	Lys	Ile	Leu	Gly	Lys	Lys	Tyr	Pro	Lys	Thr	Glu	
305					310					315					320	
Glu	Glu	Tyr	Lys	Ala	Ala	Phe	Gly	Asp	Ser	Ala	Ser	Ala	Pro	Phe	Asn	
				325					330					335		
Pro	Glu	Leu	Ala	Gly	Lys	Arg	Met	Lys	Ile	Glu	Ile	Ser	Lys	Thr	Trp	
			340					345					350			
Glu	Asn	Glu	Leu	Ser	Ala	Lys	Gly	Asn	Thr	Ala	Glu	Val	Trp	Asp	Asn	
		355					360					365				
Leu	Ile	Ser	Ser	Asn	Gln	Leu	Pro	Tyr	Met	Ala	Met	Leu	Arg	Asn	Leu	
	370					375						380				
Ser	Asn	Ile	Leu	Lys	Ala	Gly	Val	Ser	Asp	Thr	Thr	His	Ser	Ile	Val	
385					390					395					400	

Ile	Asn	Lys	Ile	Cys	Glu	Pro	Lys	Ala	Val	Glu	Asn	Ser	Lys	Met	Phe	
				405					410					415		
Pro	Leu	Gln	Phe	Phe	Ser	Ala	Ile	Glu	Ala	Val	Asn	Glu	Ala	Val	Thr	
			420					425					430			
Lys	Gly	Phe	Lys	Ala	Lys	Lys	Arg	Glu	Asn	Met	Asn	Leu	Lys	Gly	Gln	
		435					440					445				
Ile	Glu	Ala	Val	Lys	Glu	Val	Val	Glu	Lys	Thr	Asp	Glu	Glu	Lys	Lys	
	450					455					460					
Asp	Met	Glu	Leu	Glu	Gln	Thr	Glu	Glu	Gly	Glu	Phe	Val	Lys	Val	Asn	
465					470					475					480	
Glu	Gly	Ile	Gly	Lys	Gln	Tyr	Ile	Asn	Ser	Ile	Glu	Leu	Ala	Ile	Lys	
				485					490					495		
Ile	Ala	Val	Asn	Lys	Asn	Leu	Asp	Glu	Ile	Lys	Gly	His	Thr	Ala	Ile	
			500					505					510			
Phe	Ser	Asp	Val	Ser	Gly	Ser	Met	Ser	Thr	Ser	Met	Ser	Gly	Gly	Ala	
		515					520					525				
Lys	Lys	Tyr	Gly	Ser	Val	Arg	Thr	Cys	Leu	Glu	Cys	Ala	Leu	Val	Leu	
	530					535					540					
Gly	Leu	Met	Val	Lys	Gln	Arg	Cys	Glu	Lys	Ser	Ser	Phe	Tyr	Ile	Phe	
545					550					555					560	
Ser	Ser	Pro	Ser	Ser	Gln	Cys	Asn	Lys	Cys	Tyr	Leu	Glu	Val	Asp	Leu	
				565					570					575		
Pro	Gly	Asp	Glu	Leu	Arg	Pro	Ser	Met	Gln	Lys	Leu	Leu	Gln	Glu	Lys	
			580					585					590			
Gly	Lys	Leu	Gly	Gly	Gly	Thr	Asp	Phe	Pro	Tyr	Glu	Cys	Ile	Asp	Glu	
		595					600					605				
Trp	Thr	Lys	Asn	Lys	Thr	His	Val	Asp	Asn	Ile	Val	Ile	Leu	Ser	Asp	
	610					615					620					
Met	Met	Ile	Ala	Glu	Gly	Tyr	Ser	Asp	Ile	Asn	Val	Arg	Gly	Ser	Ser	
625					630					635					640	
Ile	Val	Asn	Ser	Ile	Lys	Lys	Tyr	Lys	Asp	Glu	Val	Asn	Pro	Asn	Ile	
				645					650					655		
Lys	Ile	Phe	Ala	Val	Asp	Leu	Glu	Gly	Tyr	Gly	Lys	Cys	Leu	Asn	Leu	
			660					665					670			
Gly	Asp	Glu	Phe	Asn	Glu	Asn	Asn	Tyr	Ile	Lys	Ile	Phe	Gly	Met	Ser	
		675					680					685				
Asp	Ser	Ile	Leu	Lys	Phe	Ile	Ser	Ala	Lys	Gln	Gly	Gly	Ala	Asn	Met	
	690					695					700					
Val	Glu	Val	Ile	Lys	Asn	Phe	Ala	Leu	Gln	Lys	Ile	Gly	Gln	Lys		
705					710					715						

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2829 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 47..2665
- (D) OTHER INFORMATION: /codon= (seq: "taa", aa: Gln)
/codon= (seq: "tag", aa: Gln)
/note= "Tetrahymena thermophila 95 kD
TRT protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TCAATACTAT TAATTAATAA ATAAAAAAAA GCAAAC TACA AAGAAA ATG TCA AGG	55
Met Ser Arg	
1	
CGT AAC TAA AAA AAG CCA TAG GCT CCT ATA GGC AAT GAA ACA AAT CTT	103
Arg Asn Gln Lys Lys Pro Gln Ala Pro Ile Gly Asn Glu Thr Asn Leu	
5 10 15	
GAT TTT GTA TTA CAA AAT CTA GAA GTT TAC AAA AGC CAG ATT GAG CAT	151
Asp Phe Val Leu Gln Asn Leu Glu Val Tyr Lys Ser Gln Ile Glu His	
20 25 30 35	
TAT AAG ACC TAG TAG TAA TAG ATC AAA GAG GAG GAT CTC AAG CTT TTA	199
Tyr Lys Thr Gln Gln Gln Gln Ile Lys Glu Glu Asp Leu Lys Leu Leu	
40 45 50	
AAG TTC AAA AAT TAA GAT TAG GAT GGA AAC TCT GGC AAC GAT GAT GAT	247
Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn Asp Asp Asp	
55 60 65	
GAT GAA GAA AAC AAC TCA AAT AAA TAA TAA GAA TTA TTA AGG AGA GTC	295
Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu Arg Arg Val	
70 75 80	
AAT TAG ATT AAG TAG CAA GTT TAA TTG ATA AAA AAA GTT GGT TCT AAG	343
Asn Gln Ile Lys Gln Gln Val Gln Leu Ile Lys Lys Val Gly Ser Lys	
85 90 95	
GTA GAG AAA GAT TTG AAT TTG AAC GAA GAT GAA AAC AAA AAG AAT GGA	391
Val Glu Lys Asp Leu Asn Leu Asn Glu Asp Glu Asn Lys Lys Asn Gly	
100 105 110 115	
CTT TCT GAA TAG CAA GTG AAA GAA GAG TAA TTA AGA ACG ATT ACT GAA	439
Leu Ser Glu Gln Gln Val Lys Glu Glu Gln Leu Arg Thr Ile Thr Glu	
120 125 130	
GAA TAG GTT AAG TAT TAA AAT TTA GTA TTT AAC ATG GAC TAC CAG TTA	487
Glu Gln Val Lys Tyr Gln Asn Leu Val Phe Asn Met Asp Tyr Gln Leu	
135 140 145	

GAT Asp	TTA Leu	AAT Asn 150	GAG Glu	AGT Ser	GGT Gly	GGC Gly 155	CAT His 155	AGA Arg	AGA Arg	CAC His 160	AGA Arg 160	GAA Glu	ACA Thr	GAT Asp	535	
TAT Tyr 165	GAT Asp 165	ACT Thr	GAA Glu	AAA Lys	TGG Trp	TTT Phe 170	GAA Glu	ATA Ile	TCT Ser	CAT His 175	GAC Asp 175	CAA Gln	AAA Lys	AAT Asn	TAT Tyr	583
GTA Val 180	TCA Ser	ATT Ile	TAC Tyr	GCC Ala	AAC Asn 185	TAA Gln	AAG Lys	ACA Thr	TCA Ser	TAT Tyr 190	TGT Cys 190	TGG Trp	TGG Trp	CTT Leu	AAA Lys 195	631
GAT Asp	TAT Tyr	TTT Phe	AAT Asn 200	AAA Lys 200	AAC Asn	AAT Asn	TAT Tyr	GAT Asp 205	CAT His 205	CTT Leu	AAT Asn	GTA Val	AGC Ser	ATT Ile 210	AAC Asn	679
AGA Arg	CTA Leu	GAA Glu 215	ACT Thr 215	GAA Glu	GCC Ala	GAA Glu	TTC Phe 220	TAT Tyr 220	GCC Ala	TTT Phe	GAT Asp 225	GAT Asp 225	TTT Phe	TCA Ser	CAA Gln	727
ACA Thr	ATC Ile 230	AAA Lys 230	CTT Leu	ACT Thr	AAT Asn	AAT Asn	TCT Ser 235	TAC Tyr	TAG Gln	ACT Thr	GTT Val 240	AAC Asn	ATA Ile	GAC Asp	GTT Val	775
AAT Asn 245	TTT Phe 245	GAT Asp	AAT Asn	AAT Asn	CTC Leu	TGT Cys 250	ATA Ile	CTC Leu	GCA Ala	TTG Leu 255	CTT Leu 255	AGA Arg	TTT Phe	TTA Leu	TTA Leu	823
TCA Ser 260	CTA Leu	GAA Glu	AGA Arg	TTC Phe 265	AAT Asn 265	ATT Ile	TTG Leu	AAT Asn	ATA Ile	AGA Arg 270	TCT Ser	TCT Ser	TAT Tyr	ACA Thr	AGA Arg 275	871
AAT Asn	TAA Gln	TAT Tyr	AAT Asn 280	TTT Phe 280	GAG Glu	AAA Lys	ATT Ile	GGT Gly	GAG Glu 285	CTA Leu 285	CTT Leu	GAA Glu	ACT Thr	ATC Ile 290	TTC Phe	919
GCA Ala	GTT Val	GTC Val 295	TTT Phe 295	TCT Ser	CAT His	CGC Arg	CAC His 300	TTA Leu 300	CAA Gln	GGC Gly	ATT Ile	CAT His 305	TTA Leu	CAA Gln	GTT Val	967
CCT Pro	TGC Cys 310	GAA Glu	GCG Ala	TTC Phe	TAA Gln	TAT Tyr	TTA Leu 315	GTT Val	AAC Asn	TCC Ser	TCA Ser 320	TCA Ser 320	TAA Gln	ATT Ile	AGC Ser	1015
GTT Val 325	AAA Lys 325	GAT Asp	AGC Ser	TAA Gln	TTA Leu	TAG Gln 330	GTA Val	TAC Tyr	TCT Ser	TTC Phe 335	TCT Ser 335	ACA Thr	GAC Asp	TTA Leu	AAA Lys	1063
TTA Leu 340	GTT Val	GAC Asp	ACT Thr	AAC Asn	AAA Lys 345	GTC Val	CAA Gln	GAT Asp	TAT Tyr	TTT Phe 350	AAG Lys	TTC Phe	TTA Leu	TAA Gln	GAA Glu 355	1111
TTC Phe	CCT Pro	CGT Arg	TTG Leu	ACT Thr 360	CAT His	GTA Val	AGC Ser	TAG Gln	TAG Gln 365	GCT Ala	ATC Ile	CCA Pro	GTT Val	AGT Ser	GCT Ala 370	1159
ACT Thr	AAC Asn	GCT Ala	GTA Val 375	GAG Glu	AAC Asn	CTC Leu	AAT Asn	GTT Val 380	TTA Leu	CTT Leu	AAA Lys	AAG Lys	GTC Val 385	AAG Lys	CAT His	1207

GCT AAT CTT AAT TTA GTT TCT ATC CCT ACC TAA TTC AAT TTT GAT TTC	1255
Ala Asn Leu Asn Leu Val Ser Ile Pro Thr Gln Phe Asn Phe Asp Phe	
390 395 400	
TAC TTT GTT AAT TTA TAA CAT TTG AAA TTA GAG TTT GGA TTA GAA CCA	1303
Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly Leu Glu Pro	
405 410 415	
AAT ATT TTG ACA AAA CAA AAG CTT GAA AAT CTA CTT TTG AGT ATA AAA	1351
Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Ser Ile Lys	
420 425 430 435	
TAA TCA AAA AAT CTT AAA TTT TTA AGA TTA AAC TTT TAC ACC TAC GTT	1399
Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr Thr Tyr Val	
440 445 450	
GCT TAA GAA ACC TCC AGA AAA CAG ATA TTA AAA CAA GCT ACA ACA ATC	1447
Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala Thr Thr Ile	
455 460 465	
AAA AAT CTC AAA AAC AAT AAA AAT CAA GAA GAA ACT CCT GAA ACT AAA	1495
Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro Glu Thr Lys	
470 475 480	
GAT GAA ACT CCA AGC GAA AGC ACA AGT GGT ATG AAA TTT TTT GAT CAT	1543
Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe Phe Asp His	
485 490 495	
CTT TCT GAA TTA ACC GAG CTT GAA GAT TTC AGC GTT AAC TTG TAA GCT	1591
Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn Leu Gln Ala	
500 505 510 515	
ACC CAA GAA ATT TAT GAT AGC TTG CAC AAA CTT TTG ATT AGA TCA ACA	1639
Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile Arg Ser Thr	
520 525 530	
AAT TTA AAG AAG TTC AAA TTA AGT TAC AAA TAT GAA ATG GAA AAG AGT	1687
Asn Leu Lys Lys Phe Lys Leu Ser Tyr Lys Tyr Glu Met Glu Lys Ser	
535 540 545	
AAA ATG GAT ACA TTC ATA GAT CTT AAG AAT ATT TAT GAA ACC TTA AAC	1735
Lys Met Asp Thr Phe Ile Asp Leu Lys Asn Ile Tyr Glu Thr Leu Asn	
550 555 560	
AAT CTT AAA AGA TGC TCT GTT AAT ATA TCA AAT CCT CAT GGA AAC ATT	1783
Asn Leu Lys Arg Cys Ser Val Asn Ile Ser Asn Pro His Gly Asn Ile	
565 570 575	
TCT TAT GAA CTG ACA AAT AAA GAT TCT ACT TTT TAT AAA TTT AAG CTG	1831
Ser Tyr Glu Leu Thr Asn Lys Asp Ser Thr Phe Tyr Lys Phe Lys Leu	
580 585 590 595	
ACC TTA AAC TAA GAA TTA TAA CAC GCT AAG TAT ACT TTT AAG TAG AAC	1879
Thr Leu Asn Gln Glu Leu Gln His Ala Lys Tyr Thr Phe Lys Gln Asn	
600 605 610	
GAA TTT TAA TTT AAT AAC GTT AAA AGT GCA AAA ATT GAA TCT TCC TCA	1927
Glu Phe Gln Phe Asn Asn Val Lys Ser Ala Lys Ile Glu Ser Ser Ser	
615 620 625	

TTA GAA AGC TTA GAA GAT ATT GAT AGT CTT TGC AAA TCT ATT GCT TCT Leu Glu Ser Leu Glu Asp Ile Asp Ser Leu Cys Lys Ser Ile Ala Ser 630 635 640	1975
TGT AAA AAT TTA CAA AAT GTT AAT ATT ATC GCC AGT TTG CTC TAT CCC Cys Lys Asn Leu Gln Asn Val Asn Ile Ile Ala Ser Leu Leu Tyr Pro 645 650 655	2023
AAC AAT ATT TAG AAA AAT CCT TTC AAT AAG CCC AAT CTT CTA TTT TTC Asn Asn Ile Gln Lys Asn Pro Phe Asn Lys Pro Asn Leu Leu Phe Phe 660 665 670 675	2071
AAG CAA TTT GAA TAA TTG AAA AAT TTG GAA AAT GTA TCT ATC AAC TGT Lys Gln Phe Glu Gln Leu Lys Asn Leu Glu Asn Val Ser Ile Asn Cys 680 685 690	2119
ATT CTT GAT CAG CAT ATA CTT AAT TCT ATT TCA GAA TTC TTA GAA AAG Ile Leu Asp Gln His Ile Leu Asn Ser Ile Ser Glu Phe Leu Glu Lys 695 700 705	2167
AAT AAA AAA ATA AAA GCA TTC ATT TTG AAA AGA TAT TAT TTA TTA CAA Asn Lys Lys Ile Lys Ala Phe Ile Leu Lys Arg Tyr Tyr Leu Leu Gln 710 715 720	2215
TAT TAT CTT GAT TAT ACT AAA TTA TTT AAA ACA CTT CAA TAG TTA CCT Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln Gln Leu Pro 725 730 735	2263
GAA TTA AAT TAA GTT TAC ATT AAT TAG CAA TTA GAA GAA TTG ACT GTG Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu Leu Thr Val 740 745 750 755	2311
AGT GAA GTA CAT AAG TAA GTA TGG GAA AAC CAC AAG CAA AAA GCT TTC Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln Lys Ala Phe 760 765 770	2359
TAT GAA CCA TTA TGT GAG TTT ATC AAA GAA TCA TCC TAA ACC CTT TAG Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln Thr Leu Gln 775 780 785	2407
CTA ATA GAT TTT GAC CAA AAC ACT GTA AGT GAT GAC TCT ATT AAA AAG Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser Ile Lys Lys 790 795 800	2455
ATT TTA GAA TCT ATA TCT GAG TCT AAG TAT CAT CAT TAT TTG AGA TTG Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr Leu Arg Leu 805 810 815	2503
AAC CCT AGT TAA TCT AGC AGT TTA ATT AAA TCT GAA AAC GAA GAA ATT Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn Glu Glu Ile 820 825 830 835	2551
TAA GAA CTT CTC AAA GCT TGC GAC GAA AAA GGT GTT TTA GTA AAA GCA Gln Glu Leu Leu Lys Ala Cys Asp Glu Lys Gly Val Leu Val Lys Ala 840 845 850	2599
TAC TAT AAA TTC CCT CTA TGT TTA CCA ACT GGT ACT TAT TAC GAT TAC Tyr Tyr Lys Phe Pro Leu Cys Leu Pro Thr Gly Thr Tyr Tyr Asp Tyr 855 860 865	2647

AAT TCA GAT AGA TGG TGATTAATTA AATATTAGTT TAAATAAATA TTAAATATTG	2702
Asn Ser Asp Arg Trp	
870	
AATATTTCTT TGCTTATTAT TTGAATAATA CATACAATAG TCATTTTCTAG TGTTTTGAAT	2762
ATATTTTAGT TATTTAATTC ATTATTTTAA GTAAATAATT ATTTTCAAT CATTTTAA	2822
AAAATCG	2829

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Ser	Arg	Arg	Asn	Gln	Lys	Lys	Pro	Gln	Ala	Pro	Ile	Gly	Asn	Glu	1	5	10	15
Thr	Asn	Leu	Asp	Phe	Val	Leu	Gln	Asn	Leu	Glu	Val	Tyr	Lys	Ser	Gln	20	25	30	
Ile	Glu	His	Tyr	Lys	Thr	Gln	Gln	Gln	Gln	Ile	Lys	Glu	Glu	Asp	Leu	35	40	45	
Lys	Leu	Leu	Lys	Phe	Lys	Asn	Gln	Asp	Gln	Asp	Gly	Asn	Ser	Gly	Asn	50	55	60	
Asp	Asp	Asp	Asp	Glu	Glu	Asn	Asn	Ser	Asn	Lys	Gln	Gln	Glu	Leu	Leu	65	70	75	80
Arg	Arg	Val	Asn	Gln	Ile	Lys	Gln	Gln	Val	Gln	Leu	Ile	Lys	Lys	Val	85	90	95	
Gly	Ser	Lys	Val	Glu	Lys	Asp	Leu	Asn	Leu	Asn	Glu	Asp	Glu	Asn	Lys	100	105	110	
Lys	Asn	Gly	Leu	Ser	Glu	Gln	Gln	Val	Lys	Glu	Glu	Gln	Leu	Arg	Thr	115	120	125	
Ile	Thr	Glu	Glu	Gln	Val	Lys	Tyr	Gln	Asn	Leu	Val	Phe	Asn	Met	Asp	130	135	140	
Tyr	Gln	Leu	Asp	Leu	Asn	Glu	Ser	Gly	Gly	His	Arg	Arg	His	Arg	Arg	145	150	155	160
Glu	Thr	Asp	Tyr	Asp	Thr	Glu	Lys	Trp	Phe	Glu	Ile	Ser	His	Asp	Gln	165	170	175	
Lys	Asn	Tyr	Val	Ser	Ile	Tyr	Ala	Asn	Gln	Lys	Thr	Ser	Tyr	Cys	Trp	180	185	190	
Trp	Leu	Lys	Asp	Tyr	Phe	Asn	Lys	Asn	Asn	Tyr	Asp	His	Leu	Asn	Val	195	200	205	

Ser Ile Asn Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp
 210 215 220
 Phe Ser Gln Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn
 225 230 235 240
 Ile Asp Val Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg
 245 250 255
 Phe Leu Leu Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser
 260 265 270
 Tyr Thr Arg Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu
 275 280 285
 Thr Ile Phe Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His
 290 295 300
 Leu Gln Val Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Ser
 305 310 315 320
 Gln Ile Ser Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr
 325 330 335
 Asp Leu Lys Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe
 340 345 350
 Leu Gln Glu Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro
 355 360 365
 Val Ser Ala Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys
 370 375 380
 Val Lys His Ala Asn Leu Asn Leu Val Ser Ile Pro Thr Gln Phe Asn
 385 390 395 400
 Phe Asp Phe Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly
 405 410 415
 Leu Glu Pro Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Leu
 420 425 430
 Ser Ile Lys Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr
 435 440 445
 Thr Tyr Val Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala
 450 455 460
 Thr Thr Ile Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro
 465 470 475 480
 Glu Thr Lys Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe
 485 490 495
 Phe Asp His Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn
 500 505 510
 Leu Gln Ala Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile
 515 520 525

Arg	Ser	Thr	Asn	Leu	Lys	Lys	Phe	Lys	Leu	Ser	Tyr	Lys	Tyr	Glu	Met	
530						535					540					
Glu	Lys	Ser	Lys	Met	Asp	Thr	Phe	Ile	Asp	Leu	Lys	Asn	Ile	Tyr	Glu	
545					550					555					560	
Thr	Leu	Asn	Asn	Leu	Lys	Arg	Cys	Ser	Val	Asn	Ile	Ser	Asn	Pro	His	
				565					570					575		
Gly	Asn	Ile	Ser	Tyr	Glu	Leu	Thr	Asn	Lys	Asp	Ser	Thr	Phe	Tyr	Lys	
			580					585					590			
Phe	Lys	Leu	Thr	Leu	Asn	Gln	Glu	Leu	Gln	His	Ala	Lys	Tyr	Thr	Phe	
		595					600					605				
Lys	Gln	Asn	Glu	Phe	Gln	Phe	Asn	Asn	Val	Lys	Ser	Ala	Lys	Ile	Glu	
	610					615					620					
Ser	Ser	Ser	Leu	Glu	Ser	Leu	Glu	Asp	Ile	Asp	Ser	Leu	Cys	Lys	Ser	
625					630					635					640	
Ile	Ala	Ser	Cys	Lys	Asn	Leu	Gln	Asn	Val	Asn	Ile	Ile	Ala	Ser	Leu	
				645					650					655		
Leu	Tyr	Pro	Asn	Asn	Ile	Gln	Lys	Asn	Pro	Phe	Asn	Lys	Pro	Asn	Leu	
			660					665					670			
Leu	Phe	Phe	Lys	Gln	Phe	Glu	Gln	Leu	Lys	Asn	Leu	Glu	Asn	Val	Ser	
		675					680					685				
Ile	Asn	Cys	Ile	Leu	Asp	Gln	His	Ile	Leu	Asn	Ser	Ile	Ser	Glu	Phe	
	690					695					700					
Leu	Glu	Lys	Asn	Lys	Lys	Ile	Lys	Ala	Phe	Ile	Leu	Lys	Arg	Tyr	Tyr	
705					710					715					720	
Leu	Leu	Gln	Tyr	Tyr	Leu	Asp	Tyr	Thr	Lys	Leu	Phe	Lys	Thr	Leu	Gln	
			725						730					735		
Gln	Leu	Pro	Glu	Leu	Asn	Gln	Val	Tyr	Ile	Asn	Gln	Gln	Leu	Glu	Glu	
			740					745					750			
Leu	Thr	Val	Ser	Glu	Val	His	Lys	Gln	Val	Trp	Glu	Asn	His	Lys	Gln	
		755					760					765				
Lys	Ala	Phe	Tyr	Glu	Pro	Leu	Cys	Glu	Phe	Ile	Lys	Glu	Ser	Ser	Gln	
	770					775					780					
Thr	Leu	Gln	Leu	Ile	Asp	Phe	Asp	Gln	Asn	Thr	Val	Ser	Asp	Asp	Ser	
785					790					795					800	
Ile	Lys	Lys	Ile	Leu	Glu	Ser	Ile	Ser	Glu	Ser	Lys	Tyr	His	His	Tyr	
			805						810					815		
Leu	Arg	Leu	Asn	Pro	Ser	Gln	Ser	Ser	Ser	Leu	Ile	Lys	Ser	Glu	Asn	
			820					825					830			
Glu	Glu	Ile	Gln	Glu	Leu	Leu	Lys	Ala	Cys	Asp	Glu	Lys	Gly	Val	Leu	
		835					840					845				

Val Lys Ala Tyr Tyr Lys Phe Pro Leu Cys Leu Pro Thr Gly Thr Tyr
850 855 860

Tyr Asp Tyr Asn Ser Asp Arg Trp
865 870

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 884 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..884
- (D) OTHER INFORMATION: /note= "Saccharomyces cerevisiae
L8543.12 (Est2p) protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Lys Ile Leu Phe Glu Phe Ile Gln Asp Lys Leu Asp Ile Asp Leu
1 5 10 15

Gln Thr Asn Ser Thr Tyr Lys Glu Asn Leu Lys Cys Gly His Phe Asn
20 25 30

Gly Leu Asp Glu Ile Leu Thr Thr Cys Phe Ala Leu Pro Asn Ser Arg
35 40 45

Lys Ile Ala Leu Pro Cys Leu Pro Gly Asp Leu Ser His Lys Ala Val
50 55 60

Ile Asp His Cys Ile Ile Tyr Leu Leu Thr Gly Glu Leu Tyr Asn Asn
65 70 75 80

Val Leu Thr Phe Gly Tyr Lys Ile Ala Arg Asn Glu Asp Val Asn Asn
85 90 95

Ser Leu Phe Cys His Ser Ala Asn Val Asn Val Thr Leu Leu Lys Gly
100 105 110

Ala Ala Trp Lys Met Phe His Ser Leu Val Gly Thr Tyr Ala Phe Val
115 120 125

Asp Leu Leu Ile Asn Tyr Thr Val Ile Gln Phe Asn Gly Gln Phe Phe
130 135 140

Thr Gln Ile Val Gly Asn Arg Cys Asn Glu Pro His Leu Pro Pro Lys
145 150 155 160

Trp Val Gln Arg Ser Ser Ser Ser Ser Ala Thr Ala Ala Gln Ile Lys
165 170 175

Gln Leu Thr Glu Pro Val Thr Asn Lys Gln Phe Leu His Lys Leu Asn
 180 185 190
 Ile Asn Ser Ser Ser Phe Phe Pro Tyr Ser Lys Ile Leu Pro Ser Ser
 195 200 205
 Ser Ser Ile Lys Lys Leu Thr Asp Leu Arg Glu Ala Ile Phe Pro Thr
 210 215 220
 Asn Leu Val Lys Ile Pro Gln Arg Leu Lys Val Arg Ile Asn Leu Thr
 225 230 235 240
 Leu Gln Lys Leu Leu Lys Arg His Lys Arg Leu Asn Tyr Val Ser Ile
 245 250 255
 Leu Asn Ser Ile Cys Pro Pro Leu Glu Gly Thr Val Leu Asp Leu Ser
 260 265 270
 His Leu Ser Arg Gln Ser Pro Lys Glu Arg Val Leu Lys Phe Ile Ile
 275 280 285
 Val Ile Leu Gln Lys Leu Leu Pro Gln Glu Met Phe Gly Ser Lys Lys
 290 295 300
 Asn Lys Gly Lys Ile Ile Lys Asn Leu Asn Leu Leu Leu Ser Leu Pro
 305 310 315 320
 Leu Asn Gly Tyr Leu Pro Phe Asp Ser Leu Leu Lys Lys Leu Arg Leu
 325 330 335
 Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys His
 340 345 350
 Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp Leu
 355 360 365
 Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr
 370 375 380
 Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr Trp
 385 390 395 400
 Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr Leu
 405 410 415
 Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser Asn
 420 425 430
 Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu
 435 440 445
 Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu Phe
 450 455 460
 Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln Lys
 465 470 475 480
 Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys Ile
 485 490 495

Tyr	Ser	Pro	Thr	Gln	Ile	Ala	Asp	Arg	Ile	Lys	Glu	Phe	Lys	Gln	Arg		
			500					505					510				
Leu	Leu	Lys	Lys	Phe	Asn	Asn	Val	Leu	Pro	Glu	Leu	Tyr	Phe	Met	Lys		
		515					520					525					
Phe	Asp	Val	Lys	Ser	Cys	Tyr	Asp	Ser	Ile	Pro	Arg	Met	Glu	Cys	Met		
	530					535					540						
Arg	Ile	Leu	Lys	Asp	Ala	Leu	Lys	Asn	Glu	Asn	Gly	Phe	Phe	Val	Arg		
545					550					555					560		
Ser	Gln	Tyr	Phe	Phe	Asn	Thr	Asn	Thr	Gly	Val	Leu	Lys	Leu	Phe	Asn		
				565					570					575			
Val	Val	Asn	Ala	Ser	Arg	Val	Pro	Lys	Pro	Tyr	Glu	Leu	Tyr	Ile	Asp		
			580					585					590				
Asn	Val	Arg	Thr	Val	His	Leu	Ser	Asn	Gln	Asp	Val	Ile	Asn	Val	Val		
		595					600					605					
Glu	Met	Glu	Ile	Phe	Lys	Thr	Ala	Leu	Trp	Val	Glu	Asp	Lys	Cys	Tyr		
	610					615					620						
Ile	Arg	Glu	Asp	Gly	Leu	Phe	Gln	Gly	Ser	Ser	Leu	Ser	Ala	Pro	Ile		
625					630					635					640		
Val	Asp	Leu	Val	Tyr	Asp	Asp	Leu	Leu	Glu	Phe	Tyr	Ser	Glu	Phe	Lys		
				645					650					655			
Ala	Ser	Pro	Ser	Gln	Asp	Thr	Leu	Ile	Leu	Lys	Leu	Ala	Asp	Asp	Phe		
			660					665					670				
Leu	Ile	Ile	Ser	Thr	Asp	Gln	Gln	Gln	Val	Ile	Asn	Ile	Lys	Lys	Leu		
		675					680					685					
Ala	Met	Gly	Gly	Phe	Gln	Lys	Tyr	Asn	Ala	Lys	Ala	Asn	Arg	Asp	Lys		
	690					695					700						
Ile	Leu	Ala	Val	Ser	Ser	Gln	Ser	Asp	Asp	Asp	Thr	Val	Ile	Gln	Phe		
705					710					715					720		
Cys	Ala	Met	His	Ile	Phe	Val	Lys	Glu	Leu	Glu	Val	Trp	Lys	His	Ser		
				725					730					735			
Ser	Thr	Met	Asn	Asn	Phe	His	Ile	Arg	Ser	Lys	Ser	Ser	Lys	Gly	Ile		
			740					745					750				
Phe	Arg	Ser	Leu	Ile	Ala	Leu	Phe	Asn	Thr	Arg	Ile	Ser	Tyr	Lys	Thr		
		755					760					765					
Ile	Asp	Thr	Asn	Leu	Asn	Ser	Thr	Asn	Thr	Val	Leu	Met	Gln	Ile	Asp		
	770					775					780						
His	Val	Val	Lys	Asn	Ile	Ser	Glu	Cys	Tyr	Lys	Ser	Ala	Phe	Lys	Asp		
785					790					795					800		
Leu	Ser	Ile	Asn	Val	Thr	Gln	Asn	Met	Gln	Phe	His	Ser	Phe	Leu	Gln		
				805					810					815			

Arg Ile Ile Glu Met Thr Val Ser Gly Cys Pro Ile Thr Lys Cys Asp
820 825 830

Pro Leu Ile Glu Tyr Glu Val Arg Phe Thr Ile Leu Asn Gly Phe Leu
835 840 845

Glu Ser Leu Ser Ser Asn Thr Ser Lys Phe Lys Asp Asn Ile Ile Leu
850 855 860

Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Ile Tyr Ile
865 870 875 880

His Ile Val Asn

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

YARACHAARG GHATYCCHYA RGG

23

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

DGTDATNARN ARRTARTCRT C

21

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu Cys Val Ser Tyr Ile Leu Ser Ser Phe Tyr Tyr Ala Asn Leu Glu
1 5 10 15
Glu Asn Ala Leu Gln Phe Leu Arg Lys Glu Ser Met Asp Pro Glu Lys
20 25 30
Pro Glu Thr Asn Leu Leu Met Arg Leu Thr
35 40

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu
1 5 10 15
Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn
20 25 30
Pro Asn Val Asn Leu Leu Met Arg Leu Thr
35 40

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified_base
(B) LOCATION: 1
(D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = thymidine modified by a
biotin group"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
(B) LOCATION: 12..13
(D) OTHER INFORMATION: /mod_base= gm

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 14..17
 (D) OTHER INFORMATION: /mod_base= um

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 18..21
 (D) OTHER INFORMATION: /mod_base= gm

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 22..25
 (D) OTHER INFORMATION: /mod_base= um

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 26
 (D) OTHER INFORMATION: /mod_base= gm

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

NAGACCTGTT ANNNNNNNNNN NNNNNN

26

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGGGTTTTGG GGT

16

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..389
 (D) OTHER INFORMATION: /note= "partial sequence of a cDNA
 encoding human telomerase peptide
 motifs (EST AA281296)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GCCAAGTTCC TGC	ACTGGCT	GATGAGTGTG	TACGTCGTCG	AGCTGCTCAG	GTCTTTCTTT	60
TATGTCACGG	AGACCACGTT	TCAAAAGAAC	AGGCTCTTTT	TCTACCGGAA	GAGTGTCTGG	120
AGCAAGTTGC	AAAGCATTGG	AATCAGACAG	CACTTGAAGA	GGGTGCAGCT	GCGGGACGTG	180
TCGGAAGCAG	AGGTCAGGCA	GCATCGGGAA	GCCAGGCCCG	CCCTGCTGAC	GTCCAGACTC	240
CGCTTCATCC	CCAAGCCTGA	CGGGCTGCGG	CCGATTGTGA	ACATGGACTA	CGTCGTGGGA	300
GCCAGAACGT	TCCGCAGAGA	AAAGAGGGCC	GAGCGTCTCA	CCTCGAGGGT	GAAGGCACTG	360
TTCAGCGTGC	TCAACTACGA	GCGGGCGCG				389

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ile	Ser	Glu	Ile	Glu	Trp	Leu	Val	Leu	Gly	Lys	Arg	Ser	Asn	Ala	Lys	1	5	10	15
Met	Cys	Leu	Ser	Asp	Phe	Glu	Lys	Arg	Lys	Gln	Ile	Phe	Ala	Glu	Phe	20	25	30	
Ile	Tyr	Trp	Leu	Tyr	Asn	Ser	Phe	Ile	Ile	Pro	Ile	Leu	Gln	Ser	Phe	35	40	45	
Phe	Tyr	Ile	Thr	Glu	Ser	Ser	Asp	Leu	Arg	Asn	Arg	Thr	Val	Tyr	Phe	50	55	60	
Arg	Lys	Asp	Ile	Trp	Lys	Leu	Leu	Cys	Arg	Pro	Phe	Ile	Thr	Ser	Met	65	70	75	80
Lys	Met	Glu	Ala	Phe	Glu	Lys	Ile	Asn	Glu	Asn	Asn	Val	Arg	Met	Asp	85	90	95	
Thr	Gln	Lys	Thr	Thr	Leu	Pro	Pro	Ala	Val	Ile	Arg	Leu	Leu	Pro	Lys	100	105	110	
Lys	Asn	Thr	Phe	Arg	Leu	Ile	Thr	Asn	Leu	Arg	Lys	Arg	Phe	Leu	Ile	115	120	125	
Lys	Met	Gly	Ser	Asn	Lys	Lys	Met	Leu	Val	Ser	Thr	Asn	Gln	Thr	Leu	130	135	140	
Arg	Pro	Val	Ala	Ser	Ile	Leu	Lys	His	Leu	Ile	Asn	Glu	Glu	Ser	Ser	145	150	155	160

Arg Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met
180 185 190

Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys
195 200 205

Met Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val
210 215 220

Arg Ser Gln Tyr Phe Phe Asn Thr Asn
225 230

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Thr Arg Glu Ile Ser Trp Met Gln Val Glu Thr Ser Ala Lys His Phe
1 5 10 15

Tyr Tyr Phe Asp His Glu Asn Ile Tyr Val Leu Trp Lys Leu Leu Arg
20 25 30

Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
35 40 45

Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
50 55 60

Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp Leu Lys Lys
65 70 75 80

Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu Glu Trp Lys Lys
85 90 95

Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr
100 105 110

Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val Asn Ser Asp
115 120 125

Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu Leu Asn Ser His
130 135 140

Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys Asp Pro Phe Gly
145 150 155 160

Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys Tyr Glu Glu Phe
165 170 175

Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu Phe Phe Ala Thr
180 185 190

Met Asp Ile Glu Lys Cys Tyr Asp Ser Val Asn Arg Glu Lys Leu Ser
195 200 205

Thr Phe Leu Lys Thr Thr Lys Leu Leu Ser Ser Asp Phe Trp Ile Met
210 215 220

Thr Ala Gln Ile Leu Lys Arg Lys Asn
225 230

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2631
- (D) OTHER INFORMATION: /note= "Saccharomyces cerevisiae Est 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATTTATACTC ATGAAAATCT TATTCGAGTT CATTCAAGAC AAGCTTGACA TTGATCTACA	60
GACCAACAGT ACTTACAAAG AAAATTTAAA ATGTGGTCAC TTCAATGGCC TCGATGAAAT	120
TCTAACTACG TGTTTCGCAC TACCAAATTC AAGAAAAATA GCATTACCAT GCCTTCCTGG	180
TGACTTAAGC CACAAAGCAG TCATTGATCA CTGCATCATT TACCTGTTGA CGGGCGAATT	240
ATACAACAAC GTACTAACAT TTGGCTATAA AATAGCTAGA AATGAAGATG TCAACAATAG	300
TCTTTTTTGC CATTCTGCAA ATGTTAACGT TACGTTACTG AAAGGCGCTG CTTGGAAAAT	360
GTTCCACAGT TTGGTCGGTA CATACGCATT CGTTGATTTA TTGATCAATT ATACAGTAAT	420
TCAATTTAAT GGGCAGTTTT TCACTCAAAT CGTGGGTAAC AGATGTAACG AACCTCATCT	480
GCCGCCCAAA TGGGTCCAAC GATCATCCTC ATCATCCGCA ACTGCTGCGC AAATCAAACA	540
ACTTACAGAA CCAGTGACAA ATAAACAATT CTTACACAAG CTCAATATAA ATTCCTCTTC	600
TTTTTTTCCT TATAGCAAGA TCCTTCCTTC ATCATCATCT ATCAAAAAGC TAACTGACTT	660
GAGAGAAGCT ATTTTCCCA CAAATTTGGT TAAATTCCT CAGAGACTAA AGGTACGAAT	720
TAATTTGACG CTGCAAAAGC TATTAAAGAG ACATAAGCGT TTGAATTACG TTTCTATTTT	780
GAATAGTATT TGCCCACCAT TGGAAGGGAC CGTATTGGAC TTGTCGCATT TGAGTAGGCA	840
ATCACCAAAG GAACGAGTCT TGAAATTTAT CATTGTTATT TTACAGAAGT TATTACCCCA	900
AGAAATGTTT GGCTCAAAGA AAAATAAAGG AAAAAATTATC AAGAATCTAA ATCTTTTATT	960

AAGTTTACCC	TTAAATGGCT	ATTTACCATT	TGATAGTTTG	TTGAAAAAGT	TAAGATTAAA	1020
GGATTTTCGG	TGGTTGTTCA	TTTCTGATAT	TTGGTTCACC	AAGCACAAAT	TTGAAAACTT	1080
GAATCAATTG	GCGATTTGTT	TCATTTCTCTG	GCTATTTAGA	CAACTAATTC	CCAAAATTAT	1140
ACAGACTTTT	TTTTACTGCA	CCGAAATATC	TTCTACAGTG	ACAATTGTTT	ACTTTAGACA	1200
TGATACTTGG	AATAAACTTA	TCACCCCTTT	TATCGTAGAA	TATTTTAAGA	CGTACTTAGT	1260
CGAAAAACAAC	GTATGTAGAA	ACCATAATAG	TTACACGTTG	TCCAATTTCA	ATCATAGCAA	1320
AATGAGGATT	ATACCAAAAA	AAAGTAATAA	TGAGTTCAGG	ATTATTGCCA	TCCCATGCAG	1380
AGGGGCAGAC	GAAGAAGAAT	TCACAATTTA	TAAGGAGAAT	CACAAAAATG	CTATCCAGCC	1440
CACTCAAAAA	ATTTTAGAAT	ACCTAAGAAA	CAAAAGGCCG	ACTAGTTTTA	CTAAAATATA	1500
TTCTCCAACG	CAAATAGCTG	ACCGTATCAA	AGAATTTAAG	CAGAGACTTT	TAAAGAAATT	1560
TAATAATGTC	TTACCAGAGC	TTTATTTTCAT	GAAATTTGAT	GTCAAATCTT	GCTATGATTC	1620
CATACCAAGG	ATGGAATGTA	TGAGGATACT	CAAGGATGCG	CTAAAAAATG	AAAATGGGTT	1680
TTTCGTTAGA	TCTCAATATT	TCTTCAATAC	CAATACAGGT	GTATTGAAGT	TATTTAATGT	1740
TGTTAACGCT	AGCAGAGTAC	CAAAACCTTA	TGAGCTATAC	ATAGATAATG	TGAGGACGGT	1800
TCATTTATCA	AATCAGGATG	TTATAAACGT	TGTAGAGATG	GAAATATTTA	AAACAGCTTT	1860
GTGGGTTGAA	GATAAGTGCT	ACATTAGAGA	AGATGGTCTT	TTTCAGGGCT	CTAGTTTATC	1920
TGCTCCGATC	GTTGATTTGG	TGTATGACGA	TCTTCTGGAG	TTTTATAGCG	AGTTTAAAGC	1980
CAGTCCTAGC	CAGGACACAT	TAATTTTAAA	ACTGGCTGAC	GATTTCCCTTA	TAATATCAAC	2040
AGACCAACAG	CAAGTGATCA	ATATCAAAAA	GCTTGCCATG	GGCGGATTTC	AAAAATATAA	2100
TGCGAAAGCC	AATAGAGACA	AAATTTTAGC	CGTAAGCTCC	CAATCAGATG	ATGATACGGT	2160
TATTCAATTT	TGTGCAATGC	ACATATTTGT	TAAAGAATTG	GAAGTTTGGA	AACATTCAAG	2220
CACAATGAAT	AATTTCCATA	TCCGTTTCGA	ATCTAGTAAA	GGGATATTTT	GAAGTTTAAT	2280
AGCGCTGTTT	AACACTAGAA	TCTCTTATAA	AACAATTGAC	ACAAATTTAA	ATTCAACAAA	2340
CACCGTTCTC	ATGCAAATTG	ATCATGTTGT	AAAGAACATT	TCGGAATGTT	ATAAATCTGC	2400
TTTTAAGGAT	CTATCAATTA	ATGTTACGCA	AAATATGCAA	TTTCATTTCG	TCTTACAACG	2460
CATCATTGAA	ATGACAGTCA	GCGGTTGTCC	AATTACGAAA	TGTGATCCTT	TAATCGAGTA	2520
TGAGGTACGA	TTCACCATAT	TGAATGGATT	TTTGGAAGC	CTATCTTCAA	ACACATCAAA	2580
ATTTAAAGAT	AATATCATTC	TTTTGAGAAA	GGAAATTCAA	CACTTGCAAG	C	2631

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```
Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
 1             5             10             15

Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu
      20             25             30

Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile
      35             40             45

Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu
      50             55             60

Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu
      65             70             75             80

Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp
      85             90             95

Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg
      100            105            110

Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg
      115            120            125

Ala
```

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(959..1216, 1273..1353, 1425..1543, 1595
..1857, 1894..2286, 2326..2396, 2436..2705, 2746
..2862, 2914..3083, 3125..3309, 3356..3504, 3546
..3759, 3797..4046, 4086..4252, 4296..4392, 4435
..4594)
- (D) OTHER INFORMATION: /note= "Saccharomyces pombe telomerase
catalytic subunit (TRT)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGTACCGATT TACTTTTCCTT TCTTCATAAG CTAATTGCTT CCTCGAACGC TCCTAAATCT	60
CTGGAAATAT TTTTACAAGA ACTCAATAAC AATACCAAGT CAAATTCCAA TATGAAGGTG	120
TTATTAGTGA TCGATAATAT TTCTATTTTA TCGGTCGTTA CCAAGTATAA GGACAAAAAG	180
AACAACCTCC TTCCCCCTAA AGACTTTTAC TTTATTAATT TACTTTTCAA ATATATTTTCG	240
GGTTCGCTTA CTTTTAATCG TGGTACTGTT TTAGCTGCTA CTTCTAGCCA ACCGCGTGTT	300
TCTACCCCGT CATTGGATAT AGCTCTTGGA GTAGCTCACA GAAATCCTTA CAAATCTTCT	360
GATGAGACTA TATTAGATTC ATTACAGTCC GTGCATATTC TTAACATGGA GCCTTACACT	420
TTAGATGAGT CACGTCGCAT GATGGAGTAT TTGGTATCAT CCAACGTTTG CCTTGAAAAG	480
GTTGATAATT ATTTGCAAAA TCATGTCCTT AGTGGTGGA ATCCGCGAAA GTTTTTTGAT	540
GCTTGACAC GTCTAGCATG ATTGAGATAT TCAAAAATTT CTATCCACTA CAACTCCTTT	600
AACGCGGTTT TATTTTTCTA TTTTCTATTC TCATGTTGTT CCAAATATGT ATCATCTCGT	660
ATTAGGCTTT TTTCCGTTTT ACTCCTGGAA TCGTACCTTT TTCACTATTC CCCCTAATGA	720
ATAATCTAAA TTAGTTTCGC TTATAATTGA TAGTAGTAGA AAGATTGGTG ATTCTACTCG	780
TGTAATGTTA TTAGTTTAAA GATACTTTGC AAAACATTTA TTAGCTATCA TTATATAAAA	840
AAAATCCTAT AATTATAAAT ATTAATCAAT ATTTGCGGTC ACTATTTATT TAAAACGTTA	900
TGATCAGTAG GACACTTTGC ATATATATAG TTATGCTTAA TGGTTACTTG TAACTTGC	958
ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG	1006
Met Thr Glu His His Thr Pro Lys Ser Arg Ile Leu Arg Phe Leu Glu	
1 5 10 15	
AAT CAA TAT GTA TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT	1054
Asn Gln Tyr Val Tyr Leu Cys Thr Leu Asn Asp Tyr Val Gln Leu Val	
20 25 30	
TTG AGA GGG TCG CCG GCA AGC TCG TAT AGC AAT ATA TGC GAA CGC TTG	1102
Leu Arg Gly Ser Pro Ala Ser Ser Tyr Ser Asn Ile Cys Glu Arg Leu	
35 40 45	
AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT CAT TCG ACT GTA	1150
Arg Ser Asp Val Gln Thr Ser Phe Ser Ile Phe Leu His Ser Thr Val	
50 55 60	
GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA	1198
Val Gly Phe Asp Ser Lys Pro Asp Glu Gly Val Gln Phe Ser Ser Pro	
65 70 75 80	
AAA TGC TCA CAG TCA GAG GTATATATAT TTTTGTTTTG ATTTTTTTCT	1246
Lys Cys Ser Gln Ser Glu	
85	
ATTCGGGATA GCTAATATAT GGGCAG CTA ATA GCG AAT GTT GTA AAA CAG ATG	1299
Leu Ile Ala Asn Val Val Lys Gln Met	
90 95	

TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA CTG ATG AAA GGG TTT Phe Asp Glu Ser Phe Glu Arg Arg Arg Asn Leu Leu Met Lys Gly Phe 100 105 110	1347
TCC ATG GTAAGGTATT CTAATTGTGA AATATTTACC TGCAATTACT GTTTCAAAGA Ser Met	1403
GATTGTATTT AACCGATAAA G AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA Asn His Glu Asp Phe Arg Ala Met His Val 115 120	1454
AAC GGA GTA CAA AAT GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA Asn Gly Val Gln Asn Asp Leu Val Ser Thr Phe Pro Asn Tyr Leu Ile 125 130 135	1502
TCT ATA CTT GAG TCA AAA AAT TGG CAA CTT TTG TTA GAA AT Ser Ile Leu Glu Ser Lys Asn Trp Gln Leu Leu Leu Glu Ile 140 145 150	1543
GTAAATACCG GTTAAGATGT TGC GCACTTT GAACAAGACT GACAAGTATA G T ATC Ile	1598
GGC AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG Gly Ser Asp Ala Met His Tyr Leu Leu Ser Lys Gly Ser Ile Phe Glu 155 160 165 170	1646
GCT CTT CCA AAT GAC AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT Ala Leu Pro Asn Asp Asn Tyr Leu Gln Ile Ser Gly Ile Pro Leu Phe 175 180 185	1694
AAA AAT AAT GTG TTT GAG GAA ACT GTG TCA AAA AAA AGA AAG CGA ACC Lys Asn Asn Val Phe Glu Glu Thr Val Ser Lys Lys Arg Lys Arg Thr 190 195 200	1742
ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA GAA GTT TCC Ile Glu Thr Ser Ile Thr Gln Asn Lys Ser Ala Arg Lys Glu Val Ser 205 210 215	1790
TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC Trp Asn Ser Ile Ser Ile Ser Arg Phe Ser Ile Phe Tyr Arg Ser Ser 220 225 230	1838
TAT AAG AAG TTT AAG CAA G GTA ACTAATA CTGTTATCCT TCATAACTAA Tyr Lys Lys Phe Lys Gln 235 240	1887
TTTTAG AT CTA TAT TTT AAC TTA CAC TCT ATT TGT GAT CGG AAC ACA Asp Leu Tyr Phe Asn Leu His Ser Ile Cys Asp Arg Asn Thr 245 250	1934
GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG CAA TTT GGA CTT ATA Val His Met Trp Leu Gln Trp Ile Phe Pro Arg Gln Phe Gly Leu Ile 255 260 265 270	1982
AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA TCA Asn Ala Phe Gln Val Lys Gln Leu His Lys Val Ile Pro Leu Val Ser 275 280 285	2030

CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT	2078
Gln Ser Thr Val Val Pro Lys Arg Leu Leu Lys Val Tyr Pro Leu Ile	
290 295 300	
GAA CAA ACA GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC	2126
Glu Gln Thr Ala Lys Arg Leu His Arg Ile Ser Leu Ser Lys Val Tyr	
305 310 315	
AAC CAT TAT TGC CCA TAT ATT GAC ACC CAC GAT GAT GAA AAA ATC CTT	2174
Asn His Tyr Cys Pro Tyr Ile Asp Thr His Asp Glu Lys Ile Leu	
320 325 330	
AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG TTT CTT CGA TCC ATT	2222
Ser Tyr Ser Leu Lys Pro Asn Gln Val Phe Ala Phe Leu Arg Ser Ile	
335 340 345 350	
CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA TTT	2270
Leu Val Arg Val Phe Pro Lys Leu Ile Trp Gly Asn Gln Arg Ile Phe	
355 360 365	
GAG ATA ATA TTA AAA G GTATTGTATA AAATTTATTA CCACTAACGA TTTTACCAG AC	
2327	
Glu Ile Ile Leu Lys	Asp
370	
CTC GAA ACT TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT	2375
Leu Glu Thr Phe Leu Lys Leu Ser Arg Tyr Glu Ser Phe Ser Leu His	
375 380 385	
TAT TTA ATG AGT AAC ATA AAG GTAATATGCC AAATTTTTTT ACCATTAATT	2426
Tyr Leu Met Ser Asn Ile Lys	
390 395	
AACAATCAG ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA AAA AGG TCA	2474
Ile Ser Glu Ile Glu Trp Leu Val Leu Gly Lys Arg Ser	
400 405	
AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT	2522
Asn Ala Lys Met Cys Leu Ser Asp Phe Glu Lys Arg Lys Gln Ile Phe	
410 415 420	
GCG GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA	2570
Ala Glu Phe Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu	
425 430 435 440	
CAA TCT TTT TTT TAT ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT	2618
Gln Ser Phe Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr	
445 450 455	
GTT TAT TTT AGA AAA GAT ATT TGG AAA CTC TTG TGC CGA CCC TTT ATT	2666
Val Tyr Phe Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile	
460 465 470	
ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG GTATTTTAAA	2715
Thr Ser Met Lys Met Glu Ala Phe Glu Lys Ile Asn Glu	
475 480 485	
GTATTTTTTG CAAAAAGCTA ATATTTTCAG AAC AAT GTT AGG ATG GAT ACT CAG	2769
Asn Asn Val Arg Met Asp Thr Gln	
490	

AAA ACT ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn 495 500 505	2817
ACC TTT CGT CTC ATT ACG AAT TTA AGA AAA AGA TTC TTA ATA AAG Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys 510 515 520	2862
GTATTAATTT TTGGTCATCA ATGTACTTTA CTTCTAATCT ATTATTAGCA G ATG GGT Met Gly 525	2919
TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val 530 535 540	2967
GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA Ala Ser Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro 545 550 555	3015
TTT AAC TTG GAG GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu 560 565 570	3063
CTT AAG CAC CGA ATG TTT GG GTAATTATAT AATGCGCGAT TCCTCATTAT Leu Lys His Arg Met Phe Gly 575 580	3113
TAATTTTGCA G G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA AAA TCC Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser 585 590	3161
TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys Lys 595 600 605	3209
AAA CTC AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile His 610 615 620 625	3257
GCA ACA AGT GAC CGA GCT ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe Ser 630 635 640	3305
TAT T GTAAGTTTAT TTTTTCATTG GAATTTTTTA ACAAATTCTT TTTTAG TT Tyr Phe	3357
GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser Met Lys Thr 645 650 655	3405
TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr Lys Ser Ser 660 665 670 675	3453
TCT GAA ATT TTT AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly His Ile Val 680 685 690	3501

AAG GTATACCAAT TGTGAATTG TAATAACACT AATGAAACTA G ATA GGA AAT Lys . Ile Gly Asn 695	3554
TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA ATT CTG TCA Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser 700 705 710	3602
TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu 715 720 725	3650
TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT Ser Phe Thr Lys Lys Lys Gly Ser Val Leu Leu Arg Val Val Asp Asp 730 735 740	3698
TTC CTC TTT ATA ACA GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT Phe Leu Phe Ile Thr Val Asn Lys Lys Asp Ala Lys Lys Phe Leu Asn 745 750 755	3746
TTA TCT TTA AGA G GTGAGTTGCT GTCATTCCTA AGTTCTAACC GTTGAAG GA Leu Ser Leu Arg Gly 760	3798
TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA ATA AAC Phe Glu Lys His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn 765 770 775 780	3846
TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC Phe Glu Asn Ser Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser 785 790 795	3894
AAG AAA AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT Lys Lys Arg Met Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu 800 805 810	3942
GAT ACA TTG TTA GCA TGT CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT Asp Thr Leu Leu Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser 815 820 825	3990
ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG AAA TCT TTT TTT TAC AAA Thr Ser Val Glu Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys 830 835 840	4038
ATT CTA AG GTATACTGTG TAACTGAATA ATAGCTGACA AATAATCAG A TCG Ile Leu Arg Ser 845	4089
AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser 850 855 860	4137
AAA TTC AAT TCT TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys 865 870 875 880	4185
ATG AGA GCA CAA GCA TAC TTA AAA AGG ATG AAG GAT ATA TTT ATT CCC Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro 885 890 895	4233

CAA AGA ATG TTC ATA ACG G GTGAGTACTT ATTTTAACTA GAAAAGTCAT Gln Arg Met Phe Ile Thr 900	4282
TAATTAACCT TAG AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA Asp Leu Leu Asn Val Ile Gly Arg Lys Ile Trp Lys 905 910	4330
AAG TTG GCC GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu Ser Ser 915 920 925 930	4378
GCA GAA GTC AAA TG GTACGTGTCG GTCTCGAGAC TTCAGCAATA TTGACACATC Ala Glu Val Lys Trp 935	4432
AG G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA CCC TCT TTC AAA Leu Phe Cys Leu Gly Met Arg Asp Gly Leu Lys Pro Ser Phe Lys 940 945 950	4480
TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr Gln Phe Gln Ser Leu Thr 955 960 965	4528
GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA Asp Leu Ile Lys Pro Leu Arg Pro Val Leu Arg Gln Val Leu Phe Leu 970 975 980	4576
CAT AGA AGA ATA GCT GAT TAATGTCATT TTCAATTTAT TATATACATC His Arg Arg Ile Ala Asp 985	4624
CTTTATTACT GGTGTCTTAA ACAATATTAT TACTAAGTAT AGCTGACCCC CAAAGCAAGC	4684
ATACTATAGG ATTTCTAGTA AAGTAAAATT AATCTCGTTA TTAGTTTTGA TTGACTTGTC	4744
TTTATCCTTA TACTTTTAAG AAAGATTGAC AGTGTTTGCT GACTACTGCC CACATGCCCA	4804
TTAAACGGGA GTGGTTAAAC ATTAAAAGTA ATACATGAGG CTAATCTCCT TTCATTTAGA	4864
ATAAGGAAAG TGTTTTCTA TAATGAATAA TGCCCGCACT AATGCAAAAA GACGAAGATT	4924
ATCTTCTAAA CAAGGGGGAT TAAGCATATC CGAAGGAAAA GAGAGTAATA TACCCAGTGT	4984
TGTTGAAGAA AGCAAGGATA ATTTGGAACA AGCTTCTGCA GATGACAGGC TAAATTTTGG	5044
TGACCGAATT TTGGTAAAAAG CCCCAGGTTA TCCATGGTGG CCGGCCTTGC TACTGAGACG	5104
AAAAGAAACT AAGGATAGTT TGAATACTAA TAGCTCATTT AATGTCTTAT ATAAGGTTTT	5164
GTTTTTTCCT GACTTCAATT TTGCATGGGT GAAAAGAAAT AGTGTTAAGC CATTATTGGA	5224
TTCCGAAATA GCCAAATTTC TTGGTTCCTC AAAGCGGAAG TCTAAAGAAC TTATTGAAGC	5284
TTATGAGGCT TCAAAAACTC CTCCTGATTT AAAGGAGGAA TCTTCCACCG ATGAGGAAAT	5344
GGATAGCTTA TCAGCTGCTG AGGAGAAGCC TAATTTTTTTG CAAAAAGAA AATATCATTG	5404
GGAGACATCT CTTGATGAAT CAGATGCGGA GAGTATCTCC AGCGGATCCT TGATGTCAAT	5464
AACTTCTATT TCTGAAATGT ATGGTCCTAC TGTCGCTTCG ACTTCTCGTA GCTCTACGCA	5524

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 988 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

Met Thr Glu His His Thr Pro Lys Ser Arg Ile Leu Arg Phe Leu Glu
 1             5             10             15

Asn Gln Tyr Val Tyr Leu Cys Thr Leu Asn Asp Tyr Val Gln Leu Val
          20             25             30

Leu Arg Gly Ser Pro Ala Ser Ser Tyr Ser Asn Ile Cys Glu Arg Leu
          35             40             45

Arg Ser Asp Val Gln Thr Ser Phe Ser Ile Phe Leu His Ser Thr Val
          50             55             60

Val Gly Phe Asp Ser Lys Pro Asp Glu Gly Val Gln Phe Ser Ser Pro
 65             70             75             80

Lys Cys Ser Gln Ser Glu Leu Ile Ala Asn Val Val Lys Gln Met Phe
          85             90             95

Asp Glu Ser Phe Glu Arg Arg Arg Asn Leu Leu Met Lys Gly Phe Ser
          100            105            110

Met Asn His Glu Asp Phe Arg Ala Met His Val Asn Gly Val Gln Asn
          115            120            125

Asp Leu Val Ser Thr Phe Pro Asn Tyr Leu Ile Ser Ile Leu Glu Ser
          130            135            140

Lys Asn Trp Gln Leu Leu Leu Glu Ile Ile Gly Ser Asp Ala Met His
          145            150            155            160

Tyr Leu Leu Ser Lys Gly Ser Ile Phe Glu Ala Leu Pro Asn Asp Asn
          165            170            175

Tyr Leu Gln Ile Ser Gly Ile Pro Leu Phe Lys Asn Asn Val Phe Glu
          180            185            190

Glu Thr Val Ser Lys Lys Arg Lys Arg Thr Ile Glu Thr Ser Ile Thr
          195            200            205

Gln Asn Lys Ser Ala Arg Lys Glu Val Ser Trp Asn Ser Ile Ser Ile
          210            215            220

Ser Arg Phe Ser Ile Phe Tyr Arg Ser Ser Tyr Lys Lys Phe Lys Gln
          225            230            235            240

Asp Leu Tyr Phe Asn Leu His Ser Ile Cys Asp Arg Asn Thr Val His
          245            250            255

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Met Trp Leu Gln Trp Ile Phe Pro Arg Gln Phe Gly Leu Ile Asn Ala
 260 265 270
 Phe Gln Val Lys Gln Leu His Lys Val Ile Pro Leu Val Ser Gln Ser
 275 280 285
 Thr Val Val Pro Lys Arg Leu Leu Lys Val Tyr Pro Leu Ile Glu Gln
 290 295 300
 Thr Ala Lys Arg Leu His Arg Ile Ser Leu Ser Lys Val Tyr Asn His
 305 310 315 320
 Tyr Cys Pro Tyr Ile Asp Thr His Asp Asp Glu Lys Ile Leu Ser Tyr
 325 330 335
 Ser Leu Lys Pro Asn Gln Val Phe Ala Phe Leu Arg Ser Ile Leu Val
 340 345 350
 Arg Val Phe Pro Lys Leu Ile Trp Gly Asn Gln Arg Ile Phe Glu Ile
 355 360 365
 Ile Leu Lys Asp Leu Glu Thr Phe Leu Lys Leu Ser Arg Tyr Glu Ser
 370 375 380
 Phe Ser Leu His Tyr Leu Met Ser Asn Ile Lys Ile Ser Glu Ile Glu
 385 390 395 400
 Trp Leu Val Leu Gly Lys Arg Ser Asn Ala Lys Met Cys Leu Ser Asp
 405 410 415
 Phe Glu Lys Arg Lys Gln Ile Phe Ala Glu Phe Ile Tyr Trp Leu Tyr
 420 425 430
 Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr Ile Thr Glu
 435 440 445
 Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys Asp Ile Trp
 450 455 460
 Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met Lys Met Glu Ala Phe
 465 470 475 480
 Glu Lys Ile Asn Glu Asn Asn Val Arg Met Asp Thr Gln Lys Thr Thr
 485 490 495
 Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg
 500 505 510
 Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys Met Gly Ser Asn
 515 520 525
 Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val Ala Ser
 530 535 540
 Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro Phe Asn
 545 550 555 560
 Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu Leu Lys
 565 570 575

His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys
 580 585 590
 Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys
 595 600 605
 Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile
 610 615 620
 His Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe
 625 630 635 640
 Ser Tyr Phe Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser
 645 650 655
 Met Lys Thr Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr
 660 665 670
 Lys Ser Ser Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly
 675 680 685
 His Ile Val Lys Ile Gly Asn Ser Gln Tyr Leu Gln Lys Val Gly Ile
 690 695 700
 Pro Gln Gly Ser Ile Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu
 705 710 715 720
 Asp Leu Ile Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys Gly Ser Val
 725 730 735
 Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys Lys
 740 745 750
 Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His
 755 760 765
 Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn Phe Glu Asn Ser
 770 775 780
 Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser Lys Lys Arg Met
 785 790 795 800
 Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu Asp Thr Leu Leu
 805 810 815
 Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser Thr Ser Val Glu
 820 825 830
 Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys Ile Leu Arg Ser
 835 840 845
 Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser
 850 855 860
 Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys
 865 870 875 880
 Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro
 885 890 895

Gln Arg Met Phe Ile Thr Asp Leu Leu Asn Val Ile Gly Arg Lys Ile
900 905 910

Trp Lys Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu
915 920 925

Ser Ser Ala Glu Val Lys Trp Leu Phe Cys Leu Gly Met Arg Asp Gly
930 935 940

Leu Lys Pro Ser Phe Lys Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr
945 950 955 960

Gln Phe Gln Ser Leu Thr Asp Leu Ile Lys Pro Leu Arg Pro Val Leu
965 970 975

Arg Gln Val Leu Phe Leu His Arg Arg Ile Ala Asp
980 985

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = guanosine modified by a
biotin group"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

NCCTATTTYT TYTAYNNNAC NGA

23

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Phe Phe Tyr Xaa Thr Glu
1 5

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CCAGATATNA DNARRAARTC RTC

23

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe, Ile or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Asp Asp Phe Leu Xaa Ile
1 5

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ACAATGMGNH TNHTNCCNAA RAA

23

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2..3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Arg Xaa Xaa Pro Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ACGAATCKNG GDATNSWRTC RTARCA

26

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Cys Tyr Asp Ser Ile Pro Arg
1 5

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAATTCTCRT ARCANSWYTT DATRTC

26

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Asp Ile Lys Ser Cys Tyr Asp
1 5

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GATTACTCCC GAAGAAAGGA TCTTTCCGTC CAATCATGAC TTTCTTAAGA AAGGACAAGC	60
AAAAAATAT TAAGTTAAAT CTAAATTAAA TTCTAATGGA TAGCCAACTT GTGTTTAGGA	120
ATTTAAAAGA CATGCTGGGA TAAAAGATAG GATACTCAGT CTTTGATAAT AAACAAATTT	180
CAGAAAAATT TGCCTAATTC ATAGAGAAAT GGAAAAATAA AGGAAGACCT CAGCTATATT	240
ATGTCACCTCT AGACATAAAG ACTTGCTAC	269

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AAACACAAGG AAGGAAGTCA AATATTCTAT TACCGTAAAC CAATATGGAA ATTAGTGAGT	60
AAATTAACTA TTGTCAAAGT AAGAATTTAG TTTTCTGAAA AGAATAAATA AATGAAAAAT	120
AATTTTTATC AAAAAATTTA GCTTGAAGAG GAGAATTTGG AAAAAGTTGA AGAAAAATTG	180
ATACCAGAAG ATTCATTTTA GAAATACCTT CAAGGAAAGC TAAGGATTAT ACCTAAAAAA	240
GGATCTTTCC GTCCAATCAT GACTTTCTTA AGAAAGGACA AGCAAAAAAA TATTAAGTTA	300
AATCTAAATT AAATTCTAAT GGATAGCCAA CTTGTGTTTA GGAATTTAAA AGACATGCTG	360
GGATAAAAGA TAGGATACTC AGTCTTTGAT AATAAACAAA TTTCAGAAAA ATTTGCCTAA	420
TTCATAGAGA AATGGAAAAA TAAAGGAAGA CCTCAGCTAT ATTATGTCAC TCTA	474

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ala Tyr Asp Thr Ile
1 5

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Phe	Phe	Tyr	Cys	Thr	Glu	Ile	Ser	Ser	Thr	Val	Thr	Ile	Val	Tyr	Phe
1				5					10					15	
Arg	His	Asp	Thr	Trp	Asn	Lys	Leu	Ile	Thr	Pro	Phe	Ile	Val	Glu	Tyr
			20				25						30		
Phe	Lys	Thr	Tyr	Leu	Val	Glu	Asn	Asn	Val	Cys	Arg	Asn	His	Asn	Ser
		35				40						45			
Tyr	Thr	Leu	Ser	Asn	Phe	Asn	His	Ser	Lys	Met	Arg	Ile	Ile	Pro	Lys
	50					55					60				
Lys	Ser	Asn	Asn	Glu	Phe	Arg	Ile	Ile	Ala	Ile	Pro	Cys	Arg	Gly	Ala
65					70				75						80
Asp	Glu	Glu	Glu	Phe	Thr	Ile	Tyr	Lys	Glu	Asn	His	Lys	Asn	Ala	Ile
				85					90					95	
Gln	Pro	Thr	Gln	Lys	Ile	Leu	Glu	Tyr	Leu	Arg	Asn	Lys	Arg	Pro	Thr
			100					105						110	
Ser	Phe	Thr	Lys	Ile	Tyr	Ser	Pro	Thr	Gln	Ile	Ala	Asp	Arg	Ile	Lys
		115					120					125			
Glu	Phe	Lys	Gln	Arg	Leu	Leu	Lys	Lys	Phe	Asn	Asn	Val	Leu	Pro	Glu
	130					135					140				
Leu	Tyr	Phe	Met	Lys	Phe	Asp	Val	Lys	Ser	Cys	Tyr	Asp			
145					150					155					

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Phe	Phe	Tyr	Val	Thr	Glu	Gln	Gln	Lys	Ser	Tyr	Ser	Lys	Thr	Tyr	Tyr
1				5					10					15	
Tyr	Arg	Lys	Asn	Ile	Trp	Asp	Val	Ile	Met	Lys	Met	Ser	Ile	Ala	Asp
			20					25					30		
Leu	Lys	Lys	Glu	Thr	Leu	Ala	Glu	Val	Gln	Glu	Lys	Glu	Val	Glu	Glu
		35					40					45			
Trp	Lys	Lys	Ser	Leu	Gly	Phe	Ala	Pro	Gly	Lys	Leu	Arg	Leu	Ile	Pro
	50					55					60				
Lys	Lys	Thr	Thr	Phe	Arg	Pro	Ile	Met	Thr	Phe	Asn	Lys	Lys	Ile	Val
65					70					75					80

Asn	Ser	Asp	Arg	Lys	Thr	Thr	Lys	Leu	Thr	Thr	Asn	Thr	Lys	Leu	Leu
				85					90					95	
Asn	Ser	His	Leu	Met	Leu	Lys	Thr	Leu	Lys	Asn	Arg	Met	Phe	Lys	Asp
			100					105					110		
Pro	Phe	Gly	Phe	Ala	Val	Phe	Asn	Tyr	Asp	Asp	Val	Met	Lys	Lys	Tyr
		115					120					125			
Glu	Glu	Phe	Val	Cys	Lys	Trp	Lys	Gln	Val	Gly	Gln	Pro	Lys	Leu	Phe
	130					135					140				
Phe	Ala	Thr	Met	Asp	Ile	Glu	Lys	Cys	Tyr	Asp					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Lys	His	Lys	Glu	Gly	Ser	Gln	Ile	Phe	Tyr	Tyr	Arg	Lys	Pro	Ile	Trp
1				5					10					15	
Lys	Leu	Val	Ser	Lys	Leu	Thr	Ile	Val	Lys	Val	Arg	Ile	Gln	Phe	Ser
		20					25						30		
Glu	Lys	Asn	Lys	Gln	Met	Lys	Asn	Asn	Phe	Tyr	Gln	Lys	Ile	Gln	Leu
	35					40						45			
Glu	Glu	Glu	Asn	Leu	Glu	Lys	Val	Glu	Glu	Lys	Leu	Ile	Pro	Glu	Asp
	50					55					60				
Ser	Phe	Gln	Lys	Tyr	Pro	Gln	Gly	Lys	Leu	Arg	Ile	Ile	Pro	Lys	Lys
65					70				75					80	
Gly	Ser	Phe	Arg	Pro	Ile	Met	Thr	Phe	Leu	Arg	Lys	Asp	Lys	Gln	Lys
			85					90						95	
Asn	Ile	Lys	Leu	Asn	Leu	Asn	Gln	Ile	Leu	Met	Asp	Ser	Gln	Leu	Val
			100					105					110		
Phe	Arg	Asn	Leu	Lys	Asp	Met	Leu	Gly	Gln	Lys	Ile	Gly	Tyr	Ser	Val
		115					120					125			
Phe	Asp	Asn	Lys	Gln	Ile	Ser	Glu	Lys	Phe	Ala	Gln	Phe	Ile	Glu	Lys
	130					135					140				
Trp	Lys	Asn	Lys	Gly	Arg	Pro	Gln	Leu	Tyr	Tyr	Val	Thr	Leu		
145					150					155					

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Gly Ile Pro Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTGAAGGCAC TGTTCAGCG

19

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTGGATGATT TCTTGTTGG

19

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATGCTCCTGC GTTTGGTGG

19

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CTGGACACTC AGCCCTTGG

19

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GGCAGGTGTG CTGGACACT

19

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TTTGATGATG CTGGCGATG

19

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGGGCTCGTC TTCTACAGG

19

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CAGCAGGAGG ATCTTGTAG

19

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TGACCCCAGG AGTGGCACG

19

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TCAAGCTGAC TCGACACCG

19

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CGGCGTGACA GGGCTGC

17

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GCTGAAGGCT GAGTGTCC

18

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TAGTCCATGT TCACAATCG

19

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2171 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 22..1716

(D) OTHER INFORMATION: /note= "DNA encoding ORF for 63 kD
hTRT protein from EcoRI-NotI insert of
clone 712562"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GCCAAGTTCC TGC	ACTGGCT G	ATG AGT GTG TAC GTC GTC GAG CTG CTC AGG	51
	Met Ser Val Tyr Val Val Glu Leu Leu Arg		
	1 5 10		
TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG CTC TTT	99		
Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe			
	15 20 25		
TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT GGA ATC AGA	147		
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg			
	30 35 40		
CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG GAA GCA GAG GTC	195		
Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val			
	45 50 55		
AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG ACG TCC AGA CTC CGC	243		
Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg			
	60 65 70		
TTC ATC CCC AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC	291		
Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr			
	75 80 85 90		
GTC GTG GGA GCC AGA ACG TTC CGC AGA GAA AAG ARG GCC GAG CGT CTC	339		
Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Xaa Ala Glu Arg Leu			
	95 100 105		
ACC TCG AGG GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG	387		
Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala			
	110 115 120		
CGG CGC CCC GGC CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC	435		
Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile			
	125 130 135		
CAC AGG GCC TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG	483		
His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro			
	140 145 150		
CCG CCT GAG CTG TAC TTT GTG AAG GTG GAT GTG ACG GGC GCG TAC GAC	531		
Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp			
	155 160 165 170		
ACC ATC CCC CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA	579		
Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys			
	175 180 185		
CCC CAG AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC	627		
Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala			
	190 195 200		

GCC ATG GGC ACG TCC GCA AGG CCT TCA AGA GCC ACG TCC TAC GTC CAG Ala Met Gly Thr Ser Ala Arg Pro Ser Arg Ala Thr Ser Tyr Val Gln 205 210 215	675
TGC CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser 220 225 230	723
CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG ATT CGG CGG Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg 235 240 245 250	771
GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG TTG GTG ACA CCT Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro 255 260 265	819
CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC CTG GTC CGA GGT GTC His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val 270 275 280	867
CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG AAG ACA GTG GTG AAC TTC Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe 285 290 295	915
CCT GTA GAA GAC GAG GCC CTG GGT GGC ACG GCT TTT GTT CAG ATG CCG Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro 300 305 310	963
GCC CAC GGC CTA TTC CCC TGG TGC GGC CTG CTG CTG GAT ACC CGG ACC Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr 315 320 325 330	1011
CTG GAG GTG CAG AGC GAC TAC TCC AGC TAT GCC CGG ACC TCC ATC AGA Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg 335 340 345	1059
GCC AGT CTC ACC TTC AAC CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg 350 355 360	1107
CGC AAA CTC TTT GGG GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu 365 370 375	1155
GAT TTG CAG GTG AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys 380 385 390	1203
ATC CTC CTG CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu 395 400 405 410	1251
CCA TTT CAT CAG CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA Pro Phe His Gln Gln Val Trp Lys Asn Pro His Phe Ser Cys Ala Ser 415 420 425	1299
TCT CTG ACA CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC Ser Leu Thr Arg Leu Pro Leu Leu Leu His Pro Glu Ser Gln Glu Arg 430 435 440	1347

AGG GAT GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA Arg Asp Val Ala Gly Gly Gln Gly Arg Arg Arg Pro Ser Ala Leu Arg 445 450 455	1395
GGC CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG Gly Arg Ala Val Ala Val Pro Pro Ser Ile Pro Ala Gln Ala Asp Ser 460 465 470	1443
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC CCA Thr Pro Cys His Leu Arg Ala Thr Pro Gly Val Thr Gln Asp Ser Pro 475 480 485 490	1491
GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC CCT GGA Asp Ala Ala Glu Ser Glu Ala Pro Gly Asp Asp Ala Asp Cys Pro Gly 495 500 505	1539
GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC CAT CCT GGA Gly Arg Ser Gln Pro Gly Thr Ala Leu Arg Leu Gln Asp His Pro Gly 510 515 520	1587
CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG ACA CCA GCA GCC Leu Met Ala Thr Arg Pro Gln Pro Gly Arg Glu Gln Thr Pro Ala Ala 525 530 535	1635
CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG AGG GGC GGC CCA CAC Leu Ser Arg Arg Ala Tyr Thr Ser Gln Gly Gly Arg Gly Gly Pro His 540 545 550	1683
CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC TGAGTGAGTG TTTGGCCGAG Pro Gly Leu His Arg Trp Glu Ser Glu Ala 555 560	1733
GCCTGCATGT CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA	1793
GGGCTGAGTG TCCAGCACAC CTGCGTTTTT ACTTCCCCAC AGGCTGGCGT TCGGTCCACC	1853
CCAGGGCCAG CTTTTCTCA CCAGGAGCCC GGCTTCCACT CCCCACATAG GAATAGTCCA	1913
TCCCCAGATT CGCCATTGTT CACCCTTCGC CCTGCCTTCC TTTGCCTTCC ACCCCCCACCA	1973
TTCAGGTGGA GACCCTGAGA AGGACCCTGG GAGCTTTGGG AATTTGGAGT GACCAAAGGT	2033
GTGCCCTGTA CACAGGCGAG GACCCTGCAC CTGGATGGGG GTCCCTGTGG GTCAAATTGG	2093
GGGGAGGTGC TGTGGGAGTA AAATACTGAA TATATGAGTT TTTCAGTTTT GGAAAAAAAA	2153
AAAAAAAAAA AAAAAAAAAA	2171

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	Tyr	Val	Thr	
1				5					10					15		
Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	Lys	Ser	Val	
			20					25					30			
Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	Leu	Lys	Arg	Val	
		35					40					45				
Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	His	Arg	Glu	Ala	
	50					55					60					
Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	Pro	Lys	Pro	Asp	
65					70					75					80	
Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val	Gly	Ala	Arg	Thr	
				85					90					95		
Phe	Arg	Arg	Glu	Lys	Xaa	Ala	Glu	Arg	Leu	Thr	Ser	Arg	Val	Lys	Ala	
			100					105					110			
Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala	Arg	Arg	Pro	Gly	Leu	Leu	
		115					120					125				
Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg	Ala	Trp	Arg	Thr	
	130					135					140					
Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro	Glu	Leu	Tyr	Phe	
145					150					155					160	
Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp	Thr	Ile	Pro	Gln	Asp	Arg	
			165						170				175			
Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	Pro	Gln	Asn	Thr	Tyr	Cys	
		180						185					190			
Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	Met	Gly	Thr	Ser	Ala	
	195						200					205				
Arg	Pro	Ser	Arg	Ala	Thr	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	Pro	Gln	
	210					215					220					
Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly	Asp	Met	
225					230					235				240		
Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu	Leu	Arg	
			245					250					255			
Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His	Ala	Lys	
		260						265					270			
Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	
		275					280					285				
Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu	Asp	Glu	Ala	
	290					295					300					
Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly	Leu	Phe	Pro	
305					310					315				320		

Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp
 325 330 335
 Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn
 340 345 350
 Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val
 355 360 365
 Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser
 370 375 380
 Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala
 385 390 395 400
 Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val
 405 410 415
 Trp Lys Asn Pro His Phe Ser Cys Ala Ser Ser Leu Thr Arg Leu Pro
 420 425 430
 Leu Leu Leu His Pro Glu Ser Gln Glu Arg Arg Asp Val Ala Gly Gly
 435 440 445
 Gln Gly Arg Arg Arg Pro Ser Ala Leu Arg Gly Arg Ala Val Ala Val
 450 455 460
 Pro Pro Ser Ile Pro Ala Gln Ala Asp Ser Thr Pro Cys His Leu Arg
 465 470 475 480
 Ala Thr Pro Gly Val Thr Gln Asp Ser Pro Asp Ala Ala Glu Ser Glu
 485 490 495
 Ala Pro Gly Asp Asp Ala Asp Cys Pro Gly Gly Arg Ser Gln Pro Gly
 500 505 510
 Thr Ala Leu Arg Leu Gln Asp His Pro Gly Leu Met Ala Thr Arg Pro
 515 520 525
 Gln Pro Gly Arg Glu Gln Thr Pro Ala Ala Leu Ser Arg Arg Ala Tyr
 530 535 540
 Thr Ser Gln Gly Gly Arg Gly Gly Pro His Pro Gly Leu His Arg Trp
 545 550 555 560
 Glu Ser Glu Ala

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCAGTGAGCA GAGTGACGAG GACTCGAGCT CAAGCTTTTT TTTTTTTTTT 50

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CCAGTGAGCA GAGTGACG 18

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAGGACTCGA GCTCAAGC 18

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CACTGATCCT TTCTTTTTCG TAAACGATAG GT 32

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CATCAATCAA ATCTTCCATA TAGAAATGAC A

31

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = 5' phosphorylated guanosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

NGGCCGTGTT GGCCTAGTTC TCTGCTC

27

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAGGAGGAGA AGAGCAGAGA ACTAGGCCAA CACGCCCC

38

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GTGTCATTTT TATATGGAAG ATTTGATTGA TG

32

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

ACCTATCGTT TACGAAAAAG AAAGGATCAG TG

32

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GAGTGACATA ATATACGTGA

20

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Phe Phe Tyr Val Thr Glu
1 5

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4029 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..4029

(D) OTHER INFORMATION: /note= "preliminary sequence of
hTRT cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GCAGCGCTGC	GTCTTGCTGC	GCACGTGGGA	AGCCCTGGCC	CCGGCCACCC	CCGCGATGCC	60
GCGCGCTCCC	CGCTGCCGAG	CCGTGCGCTC	CCTGCTGCGC	AGCCACTACC	GCGAGGTGCT	120
GCCGCTGGCC	ACGTTCTGTC	GGCGCCTGGG	GCCCCAGGGC	TGGCGGCTGG	TGCAGCGCGG	180
GGACCCGGCG	GCTTTCCGCG	CGNTGGTGGC	CCANTGCNTG	GTGTGCGTGC	CCTGGGANGN	240
ANGGCNGCCC	CCCGCCGCCC	CCTCCTTCCG	CCAGGTGTCC	TGCCTGAANG	ANCTGGTGGC	300
CCGAGTGCTG	CANANGCTGT	GCGANCGCGG	CGCGAANAAC	GTGCTGGCCT	TCGGCTTCGC	360
GCTGCTGGAC	GGGGCCCGCG	GGGGCCCCCC	CGAGGCCTTC	ACCACCAGCG	TGCGCAGCTA	420
CCTGCCCAAC	ACGGTGACCG	ACGCACTGCG	GGGGAGCGGG	GCGTGGGGGC	TGCTGCTGCG	480
CCGCGTGGGC	GACGACGTGC	TGGTTACCT	GCTGGCACGC	TGCGCGNTNT	TTGTGCTGGT	540
GGNTCCCAGC	TGCGCCTACC	ANGTGTGCGG	GCCGCCGCTG	TACCAGCTCG	GCGCTGCNAC	600
TCAGGCCCCG	CCCCCGCCAC	ACGCTANTGG	ACCCGAANGC	GTCTGGGATC	CAACGGGCCT	660
GGAACCATAG	CGTCAGGGAG	GCCGGGGTCC	CCCTGGGCTG	CCAGCCCCGG	GTGCGAGGAG	720
GCGCGGGGGC	AGTGCCAGCC	GAAGTCTGCC	GTTGCCCAAG	AGGCCCAGGC	GTGGCGCTGC	780
CCCTGAGCCG	GAGCGGACGC	CCGTTGGGCA	GGGGTCCTGG	GCCCACCCGG	GCAGGACGCC	840
TGGACCGAGT	GACCGTGGTT	TCTGTGTGGT	GTCACCTGCC	AGACCCGCCG	AAGAAGCCAC	900
CTCTTTGGAG	GGTGCGCTCT	CTGGCACGCG	CCACTCCCAC	CCATCCGTGG	GCCGCCAGCA	960
CCACGCGGGC	CCCCCATCCA	CATCGCGGCC	ACCACGTCCT	GGGACACGCC	TTGTCCCCCG	1020
GTGTACGCCG	AGACCAAGCA	CTTCCTCTAC	TCCTCAGGCG	ACAAGNACAC	TGCGNCCCTC	1080
CTTCCTACTC	AATATATCTG	AGGCCAGCC	TGACTGGCGT	TCGGGAGGTT	CGTGGAGACA	1140
NTCTTTCTGG	TTCCAGGCCT	TGGATGCCAG	GATTCCTCCG	AGGTTGCCCC	GCCTGCCCCA	1200
GCGNTACTGG	CAAATGCGGC	CCCTGTTTCT	GGAGCTGCTT	GGGAACCACG	CGCAGTGCCC	1260
CTACGGGGTG	TTCTCAAGA	CGCACTGCCC	GCTGCGAGCT	GCGGTCACCC	CAGCAGCCGG	1320
TGTCTGTGCC	CGGGAGAAGC	CCCAGGGCTC	TGTGGCGGCC	CCCAGGAGG	AGGAACACAG	1380
ACCCCCGTCG	CCTGGTGACG	CTGCTCCGCC	AGCACAGCAG	CCCCTGGCAG	GTGTACGGCT	1440
TCGTGCGGGC	CTGCCTGCGC	CGGCTGGTGC	CCCCAGGCCT	CTGGGGCTCC	AGGCACAACG	1500
AACGCCGCTT	CCTCAGGAAC	ACCAAGAAGT	TCATCTCCCT	GGGGAAGCAT	GCCAAGCTCT	1560

CGCTGCAGGA GCTGACGTGG AAGATGAGCG TGCGGGACTG CGCTTGGCTG CGCAGGAGCC	1620
CAGGGGTTGG CTGTGTTCCG GCCGCAGAGC ACCGTCTGCG TGAGGAGATC CTGGCCAAGT	1680
TCCTGCACTG GCTGATGAGT GTGTACGTCTG TCGAGCTGCT CAGGTCTTTC TTTTATGTCA	1740
CGGAGACCAC GTTTCAAAAAG AACAGGCTCT TTTTCTACCG GAAGAGTGTC TGGAGCAAGT	1800
TGCAAAGCAT TGGAATCAGA CAGCACTTGA AGAGGGTGCA GCTGCGGGAG CTGTCGGAAG	1860
CAGAGGTCAG GCAGCATCGG GAAGCCAGGC CCGCCCTGCT GACGTCCAGA CTCCGCTTCA	1920
TCCCCAAGCC TGACGGGCTG CGGCCGATTG TGAACATGGA CTACGTCTGT GGAGCCAGAA	1980
CGTTCCGCAG AGAAAAGAGG GCCGAGCGTC TCACCTCGAG GGTGAAGGCA CTGTTTCAGCG	2040
TGCTCAACTA CGAGCGGGCG CGGCGCCCCG GCCTCCTGGG CGCCTCTGTG CTGGGCCTGG	2100
ACGATATCCA CAGGGCCTGG CGCACCTTCG TGCTGCGTGT GCGGGCCCAG GACCCGCCGC	2160
CTGAGCTGTA CTTTGTCAAG GTGGATGTGA CGGGCGCGTA CGACACCATC CCCCAGGACA	2220
GGCTCACGGA GGTTCATCGC AGCATCATCA AACCCAGAA CACGTACTGC GTGCGTCGGT	2280
ATGCCGTGGT CCAGAAGGCC GCCCATGGGC ACGTCCGCAA GGCCTTCAAG AGCCACGTCT	2340
CTACCTTGAC AGACCTCCAG CCGTACATGC GACAGTTCGT GGCTCACCTG CAGGANAACA	2400
GCCCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG GCCAGCAGTG	2460
GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC CGTGCGCATC AGGGGCAAGT	2520
CCTACGTCCA GTGCCAGGGG ATCCCGCAGG GCTCCATCCT CTCCACGCTG CTCTGCAGCC	2580
TGTGCTACGG CGACATGGAG AACAAGCTGT TTGCGGGGAT TCGGCGGGAC GGGCTGCTCC	2640
TGCGTTTGGT GGATGATTTT TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC	2700
TCAGGACCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACTTG CGGAAGACAG	2760
TGGTGAACCT CCCTGTAGAA GACGAGGCCC TGGGTGGCAC GGCTTTTGTG CAGATGCCGG	2820
CCCACGGCCT ATTCCCCTGG TGCGGCCTGC TGCTGGATAC CCGGACCCTG GAGGTGCAGA	2880
GCGACTACTC CAGCTATGCC CGGACCTCCA TCAGAGCCAG TCTCACCTTC AACCGCGGCT	2940
TCAAGGCTGG GAGGAACATG CGTCGCAAAC TCTTTGGGGT CTTGCGGCTG AAGTGTACACA	3000
GCCTGTTTCT GGATTTGCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC ATCTACAAGA	3060
TCCTCCTGCT GCAGGCGTAC AGGTTTCACG CATGTGTGCT GCAGCTCCCA TTTCATCAGC	3120
AAGTTTGGA GAACCCCA TTTTTCCTGC GCGTCATCTC TGACACGGCC TCCCTCTGCT	3180
ACTCCATCCT GAAAGCCAAG AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGGCC	3240
CTCTGCCCTC CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCCTGCTC AAGCTGACTC	3300
GACACCGTGT CACCTACGTG CCACTCCTGG GGTCACCTCAG GACAGCCCAG ACGCAGCTGA	3360
GTCGGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC CGCAGCCAAC CCGGCACTGC	3420

CCTCAGACTT CAAGACCATC CTGGACTGAT GGCCACCCGC CCACAGCCAG GCCGAGAGCA	3480
GACACCAGCA GCCCTGTCAC GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCCACAC	3540
CCAGGCCCCGC ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT	3600
CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA GGGCTGAGTG	3660
TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG CTCGGCTCCA CCCCAGGGCC	3720
AGCTTTTCCT CACCAGGAGC CCGGCTTCCA CTCCCCACAT AGGAATAGTC CATCCCCAGA	3780
TTCGCCATTG TTCACCCCTC GCCCTGCCCT CCTTTGCCTT CCACCCCCAC CATCCAGGTG	3840
GAGACCCTGA GAAGGACCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG	3900
TACACAGGCG AGGACCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT GGGGGGAGGT	3960
GCTGTGGGAG TAAAATACTG AATATATGAG TTTTTCAGTT TTGAAAAAAA AAAAAAAAAA	4020
AAAAAAAAA	4029

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Arg or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Val"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

```
Lys Xaa Tyr Xaa Gln Xaa Xaa Gly Ile Pro Gln Gly Ser Xaa Leu Ser
1           5           10           15

Xaa Xaa Leu Xaa Xaa Xaa Xaa Tyr Xaa Asp Leu
          20           25
```

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 21
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = polar amino acid,
 selected from Gly, Ser, Thr, Tyr, Cys,
 Asn or Gln"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 25
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = polar amino acid,
 selected from Gly, Ser, Thr, Tyr, Cys,
 Asn or Gln"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Trp	Leu	Xaa	Tyr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Phe	Tyr
1				5					10					15	
Xaa	Thr	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Xaa	Arg	Lys
			20					25					30		
Xaa	Xaa	Trp													
		35													

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4038 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 56..3454
 (D) OTHER INFORMATION: /note= "refined hTRT DNA sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GCAGCGCTGC	GTCCTGCTGC	GCACGTGGGA	AGCCCTGGCC	CCGGCCACCC	CCGCG	ATG	58
						Met	
						1	
CCG	CGC	GCT	CCC	CGC	TGC	CGA	GCC
Pro	Arg	Ala	Pro	Arg	Cys	Arg	Ala
			5				10
							15
TAC	CGC	GAG	GTG	CTG	CCG	CTG	GCC
Tyr	Arg	Glu	Val	Leu	Pro	Leu	Ala
			20				25
							30

CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala 35 40 45	202
CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC GCA CGG CCG CCC Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro 50 55 60 65	250
CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC CTG AAG GAG CTG GTG Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val 70 75 80	298
GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC GGC GCG AAG AAC GTG CTG Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu 85 90 95	346
GCC TTC GGC TTC GCG CTG CTG GAC GGG GCC CGC GGG GGC CCC CCC GAG Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu 100 105 110	394
GCC TTC ACC ACC AGC GTG CGC AGC TAC CTG CCC AAC ACG GTG ACC GAC Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp 115 120 125	442
GCA CTG CGG GGG AGC GGG GCG TGG GGG CTG CTG CTG CGC CGC GTG GGC Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly 130 135 140 145	490
GAC GAC GTG CTG GTT CAC CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu 150 155 160	538
GTG GCT CCC AGC TGC GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln 165 170 175	586
CTC GGC GCT GCC ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro 180 185 190	634
CGA AGG CGT CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu 195 200 205	682
GCC GGG GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly 210 215 220 225	730
GGC AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly 230 235 240	778
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG GCC Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala 245 250 255	826
CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT GTG GTG His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val 260 265 270	874

TCA Ser 275	CCT Pro	GCC Ala	AGA Arg	CCC Pro	GCC Ala	GAA Glu	GAA Glu	GCC Ala	ACC Thr	TCT Ser	TTG Leu	GAG Glu	GGT Gly	GCG Ala	CTC Leu	922
TCT Ser 290	GGC Gly	ACG Thr	CGC Arg	CAC His	TCC Ser	CAC His	CCA Pro	TCC Ser	GTG Val	GGC Gly	CGC Arg	CAG Gln	CAC His	CAC His	GCG Ala	970
GGC Gly	CCC Pro	CCA Pro	TCC Ser	ACA Thr	TCG Ser	CGG Arg	CCA Pro	CCA Pro	CGT Arg	CCC Pro	TGG Trp	GAC Asp	ACG Thr	CCT Pro	TGT Cys	1018
CCC Pro	CCG Pro	GTG Val	TAC Tyr	GCC Ala	GAG Glu	ACC Thr	AAG Lys	CAC His	TTC Phe	CTC Leu	TAC Tyr	TCC Ser	TCA Ser	GGC Gly	GAC Asp	1066
AAG Lys	GAG Glu	CAG Gln	CTG Leu	CGG Arg	CCC Pro	TCC Ser	TTC Phe	CTA Leu	CTC Leu	AGC Ser	TCT Ser	CTG Leu	AGG Arg	CCC Pro	AGC Ser	1114
CTG Leu	ACT Thr	GGC Gly	GCT Ala	CGG Arg	AGG Arg	CTC Leu	GTG Val	GAG Glu	ACC Thr	ATC Ile	TTT Phe	CTG Leu	GGT Gly	TCC Ser	AGG Arg	1162
CCC Pro	TGG Trp	ATG Met	CCA Pro	GGG Gly	ACT Thr	CCC Pro	CGC Arg	AGG Arg	TTG Leu	CCC Pro	CGC Arg	CTG Leu	CCC Pro	CAG Gln	CGC Arg	1210
TAC Tyr	TGG Trp	CAA Gln	ATG Met	CGG Arg	CCC Pro	CTG Leu	TTT Phe	CTG Leu	GAG Glu	CTG Leu	CTT Leu	GGG Gly	AAC Asn	CAC His	GCG Ala	1258
CAG Gln	TGC Cys	CCC Pro	TAC Tyr	GGG Gly	GTG Val	CTC Leu	CTC Leu	AAG Lys	ACG Thr	CAC His	TGC Cys	CCG Pro	CTG Leu	CGA Arg	GCT Ala	1306
GCG Ala	GTC Val	ACC Thr	CCA Pro	GCA Ala	GCC Ala	GGT Gly	GTC Val	TGT Cys	GCC Ala	CGG Arg	GAG Glu	AAG Lys	CCC Pro	CAG Gln	GGC Gly	1354
TCT Ser	GTG Val	GCG Ala	GCC Ala	CCC Pro	GAG Glu	GAG Glu	GAG Glu	GAC Asp	ACA Thr	GAC Asp	CCC Pro	CGT Arg	CGC Arg	CTG Leu	GTG Val	1402
CAG Gln	CTG Leu	CTC Leu	CGC Arg	CAG Gln	CAC His	AGC Ser	AGC Ser	CCC Pro	TGG Trp	CAG Gln	GTG Val	TAC Tyr	GGC Gly	TTC Phe	GTG Val	1450
CGG Arg	GCC Ala	TGC Cys	CTG Leu	CGC Arg	CGG Arg	CTG Leu	GTG Val	CCC Pro	CCA Pro	GGC Gly	CTC Leu	TGG Trp	GGC Gly	TCC Ser	AGG Arg	1498
CAC His	AAC Asn	GAA Glu	CGC Arg	CGC Arg	TTC Phe	CTC Leu	AGG Arg	AAC Asn	ACC Thr	AAG Lys	AAG Lys	TTC Phe	ATC Ile	TCC Ser	CTG Leu	1546
GGG Gly	AAG Lys	CAT His	GCC Ala	AAG Lys	CTC Leu	TCG Ser	CTG Leu	CAG Gln	GAG Glu	CTG Leu	ACG Thr	TGG Trp	AAG Lys	ATG Met	AGC Ser	1594

GTG	CGG	GAC	TGC	GCT	TGG	CTG	CGC	AGG	AGC	CCA	GGG	GTT	GGC	TGT	GTT	1642
Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys	Val	
515						520					525					
CCG	GCC	GCA	GAG	CAC	CGT	CTG	CGT	GAG	GAG	ATC	CTG	GCC	AAG	TTC	CTG	1690
Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe	Leu	
530					535					540					545	
CAC	TGG	CTG	ATG	AGT	GTG	TAC	GTC	GTC	GAG	CTG	CTC	AGG	TCT	TTC	TTT	1738
His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	
				550					555					560		
TAT	GTC	ACG	GAG	ACC	ACG	TTT	CAA	AAG	AAC	AGG	CTC	TTT	TTC	TAC	CGG	1786
Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	
			565					570					575			
CCG	AGT	GTC	TGG	AGC	AAG	TTG	CAA	AGC	ATT	GGA	ATC	AGA	CAG	CAC	TTG	1834
Pro	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	Leu	
		580					585					590				
AAG	AGG	GTG	CAG	CTG	CGG	GAG	CTG	TCG	GAA	GCA	GAG	GTC	AGG	CAG	CAT	1882
Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	His	
	595					600					605					
CGG	GAA	GCC	AGG	CCC	GCC	CTG	CTG	ACG	TCC	AGA	CTC	CGC	TTC	ATC	CCC	1930
Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	Pro	
610					615					620					625	
AAG	CCT	GAC	GGG	CTG	CGG	CCG	ATT	GTG	AAC	ATG	GAC	TAC	GTC	GTG	GGA	1978
Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val	Gly	
				630					635					640		
GCC	AGA	ACG	TTC	CGC	AGA	GAA	AAG	AGG	GCC	GAG	CGT	CTC	ACC	TCG	AGG	2026
Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser	Arg	
			645					650					655			
GTG	AAG	GCA	CTG	TTC	AGC	GTG	CTC	AAC	TAC	GAG	CGG	GCG	CGG	CGC	CCC	2074
Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala	Arg	Arg	Pro	
		660					665					670				
GGC	CTC	CTG	GGC	GCC	TCT	GTG	CTG	GGC	CTG	GAC	GAT	ATC	CAC	AGG	GCC	2122
Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg	Ala	
	675					680				685						
TGG	CGC	ACC	TTC	GTG	CTG	CGT	GTG	CGG	GCC	CAG	GAC	CCG	CCG	CCT	GAG	2170
Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro	Glu	
690					695				700						705	
CTG	TAC	TTT	GTC	AAG	GTG	GAT	GTG	ACG	GGC	GCG	TAC	GAC	ACC	ATC	CCC	2218
Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp	Thr	Ile	Pro	
				710					715					720		
CAG	GAC	AGG	CTC	ACG	GAG	GTC	ATC	GCC	AGC	ATC	ATC	AAA	CCC	CAG	AAC	2266
Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	Pro	Gln	Asn	
			725					730					735			
ACG	TAC	TGC	GTG	CGT	CGG	TAT	GCC	GTG	GTC	CAG	AAG	GCC	GCC	CAT	GGG	2314
Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	His	Gly	
		740					745					750				

CAC	GTC	CGC	AAG	GCC	TTC	AAG	AGC	CAC	GTC	TCT	ACC	TTG	ACA	GAC	CTC	2362
His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu	Thr	Asp	Leu	
755						760					765					
CAG	CCG	TAC	ATG	CGA	CAG	TTC	GTG	GCT	CAC	CTG	CAG	GAG	ACC	AGC	CCG	2410
Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu	Thr	Ser	Pro	
770					775					780					785	
CTG	AGG	GAT	GCC	GTC	GTC	ATC	GAG	CAG	AGC	TCC	TCC	CTG	AAT	GAG	GCC	2458
Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu	Asn	Glu	Ala	
				790					795					800		
AGC	AGT	GGC	CTC	TTC	GAC	GTC	TTC	CTA	CGC	TTC	ATG	TGC	CAC	CAC	GCC	2506
Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys	His	His	Ala	
			805					810					815			
GTG	CGC	ATC	AGG	GGC	AAG	TCC	TAC	GTC	CAG	TGC	CAG	GGG	ATC	CCG	CAG	2554
Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	Pro	Gln	
		820					825					830				
GGC	TCC	ATC	CTC	TCC	ACG	CTG	CTC	TGC	AGC	CTG	TGC	TAC	GGC	GAC	ATG	2602
Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly	Asp	Met	
	835					840					845					
GAG	AAC	AAG	CTG	TTT	GCG	GGG	ATT	CGG	CGG	GAC	GGG	CTG	CTC	CTG	CGT	2650
Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu	Leu	Arg	
850					855					860					865	
TTG	GTG	GAT	GAT	TTC	TTG	TTG	GTG	ACA	CCT	CAC	CTC	ACC	CAC	GCG	AAA	2698
Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His	Ala	Lys	
				870					875					880		
ACC	TTC	CTC	AGG	ACC	CTG	GTC	CGA	GGT	GTC	CCT	GAG	TAT	GGC	TGC	GTG	2746
Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	
			885					890					895			
GTG	AAC	TTG	CGG	AAG	ACA	GTG	GTG	AAC	TTC	CCT	GTA	GAA	GAC	GAG	GCC	2794
Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu	Asp	Glu	Ala	
		900					905					910				
CTG	GGT	GGC	ACG	GCT	TTT	GTT	CAG	ATG	CCG	GCC	CAC	GGC	CTA	TTC	CCC	2842
Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly	Leu	Phe	Pro	
	915					920					925					
TGG	TGC	GGC	CTG	CTG	CTG	GAT	ACC	CGG	ACC	CTG	GAG	GTG	CAG	AGC	GAC	2890
Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val	Gln	Ser	Asp	
930					935					940					945	
TAC	TCC	AGC	TAT	GCC	CGG	ACC	TCC	ATC	AGA	GCC	AGT	GTC	ACC	TTC	AAC	2938
Tyr	Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	Arg	Ala	Ser	Val	Thr	Phe	Asn	
				950					955					960		
CGC	GGC	TTC	AAG	GCT	GGG	AGG	AAC	ATG	CGT	CGC	AAA	CTC	TTT	GGG	GTC	2986
Arg	Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	Arg	Arg	Lys	Leu	Phe	Gly	Val	
			965					970					975			
TTG	CGG	CTG	AAG	TGT	CAC	AGC	CTG	TTT	CTG	GAT	TTG	CAG	GTG	AAC	AGC	3034
Leu	Arg	Leu	Lys	Cys	His	Ser	Leu	Phe	Leu	Asp	Leu	Gln	Val	Asn	Ser	
		980					985					990				

CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG GCG Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala 995 1000 1005	3082
TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG CAA GTT Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val 1010 1015 1020 1025	3130
TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC TCT GAC ACG GCC TCC Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser 1030 1035 1040	3178
CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC GCA GGG ATG TCG CTG GGG Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly 1045 1050 1055	3226
GCC AAG GGC GCC GCC GGC CCT CTG CCC TCC GAG GCC GTG CAG TGG CTG Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu 1060 1065 1070	3274
TGC CAC CAA GCA TTC CTG CTC AAG CTG ACT CGA CAC CGT GTC ACC TAC Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr 1075 1080 1085	3322
GTG CCA CTC CTG GGG TCA CTC AGG ACA GCC CAG ACG CAG CTG AGT CGG Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg 1090 1095 1100 1105	3370
AAG CTC CCG GGG ACG ACG CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro 1110 1115 1120	3418
GCA CTG CCC TCA GAC TTC AAG ACC ATC CTG GAC TGATGGCCAC CCGCCACAG Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp 1125 1130	3471
CCAGGCCGAG AGCAGACACC AGCAGCCCTG TCACGCCGGG CTCTACGTCC CAGGGAGGGA	3531
GGGGCGGGCC ACACCCAGGC CCGCACCGCT GGGAGTCTGA GGCCTGAGTG AGTGTGTTGGC	3591
CGAGGCCTGC ATGTCCGGCT GAAGGCTGAG TGTCCGGCTG AGGCCTGAGC GAGTGTCCAG	3651
CCAAGGGCTG AGTGTCCAGC ACACCTGCCG TCTTCACTTC CCCACAGGCT GGCGCTCGGC	3711
TCCACCCCAG GGCCAGCTTT TCYTACCAG GAGCCCGGCT TCCACTCCCC ACATAGGAAT	3771
AGTCCATCCC CAGATTCGCC ATTGTTACCC CYTCGCCCTG CCYTCCTTTG CCTTCCACCC	3831
CCACCATCCA GGTGGAGACC CTGAGAAGGA CCCTGGGAGC TCTGGGAATT TGGAGTGACC	3891
AAAGGTGTGC CCTGTACACA GGCGAGGACC CTGCACCTGG ATGGGGGTCC CTGTGGGTCA	3951
AATTGGGGGG AGGTGCTGTG GGAGTAAAT ACTGAATATA TGAGTTTTTC AGTTTTGRAA	4011
AAAAAAAAAA AAAAAAAAAA AAAAAA	4038

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1132 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Met	Pro	Arg	Ala	Pro	Arg	Cys	Arg	Ala	Val	Arg	Ser	Leu	Leu	Arg	Ser	
1				5					10					15		
His	Tyr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	
			20					25					30			
Pro	Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	
		35					40					45				
Ala	Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	
	50					55				60						
Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu	
65					70					75					80	
Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	
				85					90					95		
Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	
			100					105					110			
Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	
		115					120					125				
Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	
	130					135					140					
Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	
145					150					155					160	
Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	
			165						170					175		
Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	
			180					185					190			
Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg	
		195					200					205				
Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	
	210					215					220					
Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg	
225					230					235				240		
Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp	
			245					250						255		
Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	Cys	Val	
			260				265						270			

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
275 280 285
Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
290 295 300
Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
305 310 315 320
Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
325 330 335
Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
340 345 350
Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
355 360 365
Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
370 375 380
Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
385 390 395 400
Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
405 410 415
Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
420 425 430
Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
435 440 445
Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
450 455 460
Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
465 470 475 480
Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
485 490 495
Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
500 505 510
Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
515 520 525
Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
530 535 540
Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
545 550 555 560
Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
565 570 575
Arg Pro Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800
 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815
 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
915 920 925

Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
930 935 940

Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Val Thr Phe
945 950 955 960

Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
965 970 975

Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
980 985 990

Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
995 1000 1005

Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
1010 1015 1020

Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
1025 1030 1035 1040

Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
1045 1050 1055

Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
1060 1065 1070

Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
1075 1080 1085

Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
1090 1095 1100

Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
1105 1110 1115 1120

Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
1125 1130

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
1 5 10 15

Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa
20 25 30

Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile
 35 40

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
 1 5 10 15
 Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa
 20 25 30
 Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile
 35 40

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Glu Xaa Xaa Val Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3855 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 56..2479
- (D) OTHER INFORMATION: /product= "hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCAGCGCTGC	GTCTGCTGC	GCACGTGGGA	AGCCCTGGCC	CCGGCCACCC	CCGCG	ATG	58
						Met	
						1	
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC CAC	106						
Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His							
		5				10	
						15	
TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG GGG CCC	154						
Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro							
		20				25	
						30	
CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG	202						
Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala							
		35				40	
						45	
CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC GCA CGG CCG CCC	250						
Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro							
		50				55	
						60	
						65	
CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC CTG AAG GAG CTG GTG	298						
Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val							
				70		75	
						80	
GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC GGC GCG AAG AAC GTG CTG	346						
Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu							
		85				90	
						95	
GCC TTC GGC TTC GCG CTG CTG GAC GGG GCC CGC GGG GGC CCC CCC GAG	394						
Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu							
		100				105	
						110	
GCC TTC ACC ACC AGC GTG CGC AGC TAC CTG CCC AAC ACG GTG ACC GAC	442						
Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp							
		115				120	
						125	
GCA CTG CGG GGG AGC GGG GCG TGG GGG CTG CTG CTG CGC CGC GTG GGC	490						
Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly							
		130				135	
						140	
						145	
GAC GAC GTG CTG GTT CAC CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG	538						
Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu							
				150		155	
						160	
GTG GCT CCC AGC TGC GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG	586						
Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln							
		165				170	
						175	
CTC GGC GCT GCC ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC	634						
Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro							
		180				185	
						190	
CGA AGG CGT CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG	682						
Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu							
		195				200	
						205	
GCC GGG GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG	730						
Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly							
		210				215	
						220	
						225	

GGC AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly	778
230 235 240	
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG GCC Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala	826
245 250 255	
CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT GTG GTG His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val	874
260 265 270	
TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG GGT GCG CTC Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu	922
275 280 285	
TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC CAG CAC CAC GCG Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala	970
290 295 300 305	
GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC TGG GAC ACG CCT TGT Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys	1018
310 315 320	
CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC CTC TAC TCC TCA GGC GAC Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp	1066
325 330 335	
AAG GAG CAG CTG CGG CCC TCC TTC CTA CTC AGC TCT CTG AGG CCC AGC Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser	1114
340 345 350	
CTG ACT GGC GCT CGG AGG CTC GTG GAG ACC ATC TTT CTG GGT TCC AGG Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg	1162
355 360 365	
CCC TGG ATG CCA GGG ACT CCC CGC AGG TTG CCC CGC CTG CCC CAG CGC Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg	1210
370 375 380 385	
TAC TGG CAA ATG CGG CCC CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala	1258
390 395 400	
CAG TGC CCC TAC GGG GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala	1306
405 410 415	
GCG GTC ACC CCA GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly	1354
420 425 430	
TCT GTG GCG GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val	1402
435 440 445	
CAG CTG CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val	1450
450 455 460 465	

CGG GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG	1498
Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg	
470 475 480	
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC CTG	1546
His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu	
485 490 495	
GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG ATG AGC	1594
Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser	
500 505 510	
GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT GGC TGT GTT	1642
Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val	
515 520 525	
CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG GCC AAG TTC CTG	1690
Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu	
530 535 540 545	
CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG CTC AGG TCT TTC TTT	1738
His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe	
550 555 560	
TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG CTC TTT TTC TAC CGG	1786
Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg	
565 570 575	
AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT GGA ATC AGA CAG CAC TTG	1834
Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu	
580 585 590	
AAG AGG GTG CAG CTG CGG GAG CTG TCG GAA GCA GAG GTC AGG CAG CAT	1882
Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His	
595 600 605	
CGG GAA GCC AGG CCC GCC CTG CTG ACG TCC AGA CTC CGC TTC ATC CCC	1930
Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro	
610 615 620 625	
AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA	1978
Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly	
630 635 640	
GCC AGA ACG TTC CGC AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG	2026
Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg	
645 650 655	
GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC	2074
Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro	
660 665 670	
GGC CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC	2122
Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala	
675 680 685	
TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG	2170
Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu	
690 695 700 705	

CTG TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro 710 715 720	2218
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn 725 730 735	2266
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC CAT GGG Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly 740 745 750	2314
CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC CTA CGT CCA GTG CCA GGG His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro Gly 755 760 765	2362
GAT CCC GCA GGG CTC CAT CCT CTC CAC GCT GCT CTG CAG CCT GTG CTA Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu 770 775 780 785	2410
CGG CGA CAT GGA GAA CAA GCT GTT TGC GGG GAT TCG GCG GGA CGG GCT Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala 790 795 800	2458
GCT CCT GCG TTT GGT GGA TGATTTCTTG TTGGTGACAC CTCACCTCAC Ala Pro Ala Phe Gly Gly 805	2506
CCACGCGAAA ACCTTCCTCA GGACCCTGGT CCGAGGTGTC CCTGAGTATG GCTGCGTGGT	2566
GAAGTTGCGG AAGACAGTGG TGAAGTCCCT TGTAGAAGAC GAGGCCCTGG GTGGCACGGC	2626
TTTTGTTCAG ATGCCGGCCC ACGGCCTATT CCCCTGGTGC GGCCTGCTGC TGGATACCCG	2686
GACCCTGGAG GTGCAGAGCG ACTACTCCAG CTATGCCCGG ACCTCCATCA GAGCCAGTCT	2746
CACCTTCAAC CGCGGCTTCA AGGCTGGGAG GAACATGCGT CGCAAACCTCT TTGGGGTCTT	2806
GCGGCTGAAG TGTCACAGCC TGTTTCTGGA TTTGCAGGTG AACAGCCTCC AGACGGTGTG	2866
CACCAACATC TACAAGATCC TCCTGCTGCA GCGGTACAGG TTTCACGCAT GTGTGCTGCA	2926
GCTCCCATTT CATCAGCAAAG TTTGGAAGAA CCCACATTT TTCCTGCGCG TCATCTCTGA	2986
CACGGCCTCC CTCTGCTACT CCATCCTGAA AGCCAAGAAC GCAGGGATGT CGCTGGGGGC	3046
CAAGGGCGCC GCCGGCCCTC TGCCCTCCGA GGCCGTGCAG TGGCTGTGCC ACCAAGCATT	3106
CCTGCTCAAG CTGACTCGAC ACCGTGTCAC CTACGTGCCA CTCCTGGGGT CACTCAGGAC	3166
AGCCCAGACG CAGCTGAGTC GGAAGCTCCC GGGGACGACG CTGACTGCCC TGGAGGCCGC	3226
AGCCAACCCG GCACTGCCCT CAGACTTCAA GACCATCCTG GACTGATGGC CACCCGCCCA	3286
CAGCCAGGCC GAGAGCAGAC ACCAGCAGCC CTGTCACGCC GGGCTCTACG TCCCAGGGAG	3346
GGAGGGGCGG CCCACACCCA GGCCCGCACC GCTGGGAGTC TGAGGCCTGA GTGAGTGTTT	3406
GGCCGAGGCC TGCATGTCCG GCTGAAGGCT GAGTGTCCGG CTGAGGCCTG AGCGAGTGTC	3466
CAGCCAAGGG CTGAGTGTCC AGCACACCTG CCGTCTTCAC TTCCCCACAG GCTGGCGCTC	3526

GGCTCCACCC CAGGGCCAGC TTTTCCTCAC CAGGAGCCCG GCTTCCACTC CCCACATAGG	3586
AATAGTCCAT CCCCAGATTC GCCATTGTTC ACCCCTCGCC CTGCCCTCCT TTGCCTTCCA	3646
CCCCCACCAT CCAGGTGGAG ACCCTGAGAA GGACCCTGGG AGCTCTGGGA ATTTGGAGTG	3706
ACCAAAGGTG TGCCCTGTAC ACAGGCGAGG ACCCTGCACC TGGATGGGGG TCCCTGTGGG	3766
TCAAATTGGG GGGAGGTGCT GTGGGAGTAA AATACTGAAT ATATGAGTTT TTCAGTTTTG	3826
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	3855

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Met	Pro	Arg	Ala	Pro	Arg	Cys	Arg	Ala	Val	Arg	Ser	Leu	Leu	Arg	Ser	1	5	10	15
His	Tyr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	20	25	30	
Pro	Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	35	40	45	
Ala	Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	50	55	60	
Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu	65	70	75	80
Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	85	90	95	
Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	100	105	110	
Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	115	120	125	
Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	130	135	140	
Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	145	150	155	160
Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	165	170	175	
Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	180	185	190	

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro
 755 760 765
 Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val
 770 775 780
 Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg
 785 790 795 800
 Ala Ala Pro Ala Phe Gly Gly
 805

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3025 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3025
- (D) OTHER INFORMATION: /note= "mouse TRT cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CGGGTGGGAG GCCCATCCCG GCCTTGAGCA CAATGACCCG CGCTCCTCGT TGCCCCGCGG	60
TGCGCTCTCT GCTGCGCAGC CGATACCGGG AGGTGTGGCC GCTGGCAACC TTTGTGCGGC	120
GCCTGGGGCC CGAGGGCAGG CGGCTTGTGC AACCCGGGGA CCCGAAGATC TACCGCACTT	180
TGGTTGCCCA ATGCCTAGTG TGCATGCACT GGGGCTCACA GCCTCCACCT GCCGACCTTT	240
CCTTCCACCA GGTGTCATCC CTGAAAGAGC TGGTGGCCAG GGTGTGCAG AGACTCTGCG	300
AGCGCAACGA GAGAAACGTG CTGGCTTTTG GCTTTGAGCT GCTTAACGAG GCCAGAGGCG	360
GGCCTCCCAT GGCCTTCACT AGTAGCGTGC GTAGCTACTT GCCCAACACT GTTATTGAGA	420
CCCTGCGTGT CAGTGGTGCA TGGATGCTAC TGTTGAGCCG AGTGGGCGAC GACCTGCTGG	480
TCTACCTGCT GGCACACTGT GCTCTTTATC TTCTGGTGCC CCCCAGCTGT GCCTACCAGG	540
TGTGTGGGTC TCCCCTGTAC CAAATTTGTG CCACCACGGA TATCTGGCCC TCTGTGTCCG	600
CTAGTTACAG GCCCACCCGA CCCGTGGGCA GGAATTTTAC TAACCTTAGG TTCTTACAAC	660
AGATCAAGAG CAGTAGTCGC CAGGAAGCAC CGAAACCCCT GGCCTTGCCA TCTCGAGGTA	720
CAAAGAGGCA TCTGAGTCTC ACCAGTACAA GTGTGCCTTC AGCTAAGAAG GCCAGATGCT	780
ATCCTGTCCC GAGAGTGGAG GAGGGACCCC ACAGGCAGGT GCTACCAACC CCATCAGGCA	840
AATCATGGGT GCCAAGTCCT GTCGGTCCC CCGAGGTGCC TACTGCAGAG AAAGATTTGT	900
CTTCTAAAGG AAAGGTGTCT GACCTGAGTC TCTCTGGGTC GGTGTGCTGT AAACACAAGC	960
CCAGCTCCAC ATCTCTGCTG TCACCACCCC GCCAAAATGC CTTTCAGCTC AGGCCATTTA	1020
TTGAGACCAG ACATTTCTT TACTCCAGGG GAGATGGCCA AGAGCGTCTA AACCCCTCAT	1080
TCCTACTCAG CAACCTCCAG CCTAACTTGA CTGGGGCCAG GAGACTGGTG GAGATCATCT	1140
TTCTGGGCTC AAGGCCTAGG ACATCAGGAC CACTCTGCAG GACACACCGT CTATCGCGTC	1200
GATACTGGCA GATGCGGCCC CTGTTCCAAC AGCTGCTGGT GAACCATGCA GAGTGCCAAT	1260

ATGTCAGACT	CCTCAGGTCA	CATTGCAGGT	TTCGAACAGC	AAACCAACAG	GTGACAGATG	1320
CCTTGAACAC	CAGCCCACCG	CACCTCATGG	ATTTGCTCCG	CCTGCACAGC	AGTCCCTGGC	1380
AGGTATATGG	TTTTCTTCGG	GCCTGTCTCT	GCAAGGTGGT	GTCTGCTAGT	CTCTGGGGTA	1440
CCAGGCACAA	TGAGCGCCGC	TTCTTTAAGA	ACTTAAAGAA	GTCATCTCG	TTGGGGAAAT	1500
ACGGCAAGCT	ATCACTGCAG	GAAGTATGT	GGAAGATGAA	AGTAGAGGAT	TGCCACTGGC	1560
TCCGCAGCAG	CCCGGGGAAG	GACCGTGTCC	CCGCTGCAGA	GCACCGTCTG	AGGGAGAGGA	1620
TCCTGGCTAC	GTTCTGTTC	TGGCTGATGG	ACACATACGT	GGTACAGCTG	CTTAGGTCAT	1680
TCTTTTACAT	CACAGAGAGC	ACATTCCAGA	AGAACAGGCT	CTTCTTCTAC	CGTAAGAGTG	1740
TGTGGAGCAA	GCTGCAGAGC	ATTGGAGTCA	GGCAACACCT	TGAGAGAGTG	CGGCTACGGG	1800
AGCTGTCACA	AGAGGAGGTC	AGGCATCACC	AGGACACCTG	GCTAGCCATG	CCCATCTGCA	1860
GACTGCGCTT	CATCCCCAAG	CCCAACGGCC	TGCGGCCCAT	TGTGAACATG	AGTTATAGCA	1920
TGGGTACCAG	AGCTTTGGGC	AGAAGGAAGC	AGGCCCAGCA	TTTCACCCAG	CGTCTCAAGA	1980
CTCTCTTCAG	CATGCTCAAC	TATGAGCCGA	CAAAACATCC	TCACCTTATG	GGGTCTTCTG	2040
TACTGGGTAT	GAATGACATC	TACAGGACCT	GGCGGGCCTT	TGTGCTGCGT	GTGCGTGCTC	2100
TGGACCANAC	ACCANGATGT	ACTTTGTAA	GGCAGATGTG	ACCGGGGCCT	ATGATGCCAT	2160
CCCCAGGGTA	AGCTGGGTGN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	2220
TGGTGGAGGT	TGTTGCCAAT	ATGATCAGGC	ATTGCGAGAG	CACGTACTGT	ATCCGCCAGT	2280
ATGCAGTGGT	CCGGAGAGAT	AGCCAAGGCC	AAGTCCACAA	GTCNTTTAGG	AGACAGGTCA	2340
CCACCTTCTC	TGACTTCCAG	CCATACATGG	GCCAGTTCCT	TAAGCATCTG	CAGGATTCAG	2400
ATGCCAGTGC	ACTGAGGAAC	TCCGTTGTCA	TCGAGCAGAG	CATCTCTATG	AATGAGAGCA	2460
GCAGCAGCCT	GTTTGATTCT	TCCTGCACTT	CCTGCGTCAC	AGTGTCGTAA	AGATTGGTGA	2520
CAGGTGCTAT	ACGCAGTGCC	AGGGCATCCC	CCAGGGCTCC	AGCCTATCCA	CCCTGCTCTG	2580
CAGTCTGTGT	TTCGGAGACA	TGGAGAACAA	GCTGTTTGCT	GAGGTGCAGC	GGGATGGGTT	2640
GCTTTTACGT	TTTGTTGATG	ACTTCTGTG	GGTGACGCCT	CACTTGGACC	AAGCANNNNN	2700
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	2760
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	2820
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	2880
NNNNNNNNNN	CTGCAGTTAT	GCCCAGACCT	CAATTAAGAC	GAGCCTCACC	TTCCAGAGTG	2940
TCTTCAAAGC	TGGGAAGACC	ATGCGGAACA	AGCTCCTGTC	GGTCTTGCGG	TTGAAGTGTC	3000
ACGGTCTATT	TCTAGACTTG	CAGGT				3025

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CTTTTACATC ACAGAGAGCA C

21

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CTCGGACCAG GGTCTGAGG AA

22

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Cys	Gly	Gly	Gln	Lys	Gln	Leu	Glu	Phe	Tyr	Phe	Ser	Asp	Ala	Asn	Leu
1				5				10						15	
Tyr Asn Asp Ser Phe Leu															
20															

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn
1 5 10 15
Glu Phe Arg Ile Ile
20

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Cys Leu Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr
1 5 10 15
Asp Ser Ile Pro Arg Met Glu Cys Met Arg Ile Leu Lys
20 25

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1285 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp
1 5 10 15
Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala His Trp
20 25 30
Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp
35 40 45
Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Arg Ile Asp His Asn
50 55 60
Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu
65 70 75 80
Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser
85 90 95

Lys	Gly	Gln	Leu	Lys	Glu	Phe	Leu	Asp	Ala	Asn	Leu	Ala	Gly	Ser	Gly		
			100					105					110				
Ser	Gly	Asp	Asp	Asp	Asp	Lys	Val	Pro	Met	His	Glu	Leu	Glu	Ile	Phe		
		115					120					125					
Glu	Phe	Ala	Ala	Ala	Ser	Thr	Gln	Arg	Cys	Val	Leu	Leu	Arg	Thr	Trp		
	130					135					140						
Glu	Ala	Leu	Ala	Pro	Ala	Thr	Pro	Ala	Met	Pro	Arg	Ala	Pro	Arg	Cys		
145					150					155					160		
Arg	Ala	Val	Arg	Ser	Leu	Leu	Arg	Ser	His	Tyr	Arg	Glu	Val	Leu	Pro		
				165					170					175			
Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	Pro	Gln	Gly	Trp	Arg	Leu	Val		
			180					185					190				
Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	Ala	Leu	Val	Ala	Gln	Cys	Leu		
		195					200					205					
Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	Pro	Pro	Ala	Ala	Pro	Ser	Phe		
	210					215					220						
Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg		
225					230					235					240		
Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu		
				245				250						255			
Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val		
			260				265						270				
Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly		
		275					280					285					
Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His		
	290					295				300							
Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala		
305					310					315					320		
Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln		
				325					330					335			
Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys		
			340					345					350				
Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly		
		355					360					365					
Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser		
	370					375					380						
Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu		
385					390					395					400		
Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg		
				405					410				415				

Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala
 420 425 430
 Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser
 435 440 445
 His Pro Ser Val Gly Arg Gln His His Ala Gly Pro Pro Ser Thr Ser
 450 455 460
 Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu
 465 470 475 480
 Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro
 485 490 495
 Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg
 500 505 510
 Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr
 515 520 525
 Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro
 530 535 540
 Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val
 545 550 555 560
 Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala
 565 570 575
 Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu
 580 585 590
 Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His
 595 600 605
 Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg
 610 615 620
 Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe
 625 630 635 640
 Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu
 645 650 655
 Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp
 660 665 670
 Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg
 675 680 685
 Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val
 690 695 700
 Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr
 705 710 715 720
 Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys
 725 730 735

Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg
 740 745 750
 Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala
 755 760 765
 Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg
 770 775 780
 Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg
 785 790 795 800
 Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser
 805 810 815
 Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser
 820 825 830
 Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu
 835 840 845
 Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val
 850 855 860
 Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu
 865 870 875 880
 Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg
 885 890 895
 Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe
 900 905 910
 Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln
 915 920 925
 Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val
 930 935 940
 Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp
 945 950 955 960
 Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
 965 970 975
 Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr
 980 985 990
 Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala
 995 1000 1005
 Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu
 1010 1015 1020
 Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu
 1025 1030 1035 1040
 Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr
 1045 1050 1055

Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe
 1060 1065 1070
 Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu
 1075 1080 1085
 Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg
 1090 1095 1100
 Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly
 1105 1110 1115 1120
 Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His
 1125 1130 1135
 Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr
 1140 1145 1150
 Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys
 1155 1160 1165
 Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe
 1170 1175 1180
 Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu
 1185 1190 1195 1200
 Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly
 1205 1210 1215
 Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu
 1220 1225 1230
 Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser
 1235 1240 1245
 Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr
 1250 1255 1260
 Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe
 1265 1270 1275 1280
 Lys Thr Ile Leu Asp
 1285

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
			20					25					30			
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
		35					40					45				
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
	50					55					60					
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
65					70					75					80	
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
				85					90					95		
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
			100					105					110			
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
		115					120					125				
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
	130					135					140					
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
145					150					155					160	
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
				165					170					175		
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
			180					185					190			
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
		195					200					205				
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
	210					215					220					
Gly	Ser	Arg	Arg	Ala	Ser	Val	Gly	Ser	Val	Thr	Lys	Ile	Pro	Gln	Gly	
225					230					235					240	
Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly	Asp	Met	Glu	
				245					250					255		
Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu	Leu	Arg	Leu	
		260						265					270			
Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His	Ala	Lys	Thr	
		275					280					285				
Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	Val	
	290					295					300					
Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu	Asp	Glu	Ala	Leu	
305					310					315					320	
Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly	Leu	Phe	Pro	Trp	
				325					330					335		

Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr
 340 345 350
 Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Val Thr Phe Asn Arg
 355 360 365
 Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu
 370 375 380
 Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu
 385 390 395 400
 Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr
 405 410 415
 Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp
 420 425 430
 Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu
 435 440 445
 Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala
 450 455 460
 Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys
 465 470 475 480
 His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val
 485 490 495
 Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys
 500 505 510
 Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala
 515 520 525
 Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 530 535

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 530 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	50	55	60
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	65	70	75
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	85	90	95
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	100	105	110
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	115	120	125
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	130	135	140
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	145	150	155
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	165	170	175
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	180	185	190
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	195	200	205
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	210	215	220
Gly	Ser	Arg	Arg	Ala	Ser	Val	Gly	Ser	Val	His	His	His	His	His	His	225	230	235
His	His	Gly	Ser	Val	Thr	Lys	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	245	250	255
Arg	Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	260	265	270
Phe	Phe	Tyr	Arg	Pro	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	275	280	285
Arg	Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	290	295	300
Val	Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	305	310	315
Arg	Phe	Ile	Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	325	330	335
Tyr	Val	Val	Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	340	345	350
Leu	Thr	Ser	Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	355	360	365

Ala	Arg	Arg	Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	370	375	380	
Ile	His	Arg	Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	385	390	395	400
Pro	Pro	Pro	Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	405	410	415	
Asp	Thr	Ile	Pro	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	420	425	430	
Lys	Pro	Gln	Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	435	440	445	
Ala	Ala	His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	450	455	460	
Leu	Thr	Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	465	470	475	480
Glu	Thr	Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	485	490	495	
Leu	Asn	Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	500	505	510	
Cys	His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	515	520	525	
Gly	Ile															530			

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro	1	5	10	15
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	20	25	30	
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	35	40	45	
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	50	55	60	
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	65	70	75	80

Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
				85					90					95		
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
			100					105					110			
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
		115					120					125				
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
	130					135					140					
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
145					150					155					160	
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
				165					170					175		
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
			180					185					190			
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
		195					200					205				
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
	210					215					220					
Gly	Ser	Arg	Arg	Ala	Ser	Val	Gly	Ser	Val	Thr	Lys	Met	Ser	Val	Tyr	
225					230					235					240	
Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	
				245					250					255		
Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	Pro	Ser	Val	Trp	Ser	Lys	Leu	
			260					265					270			
Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	
		275					280					285				
Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	
	290					295					300					
Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	
305					310					315					320	
Ile	Val	Asn	Met	Asp	Tyr	Val	Val	Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	
				325					330					335		
Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser	Arg	Lys	Ala	Leu	Phe	Ser	Val	Leu	
			340					345					350			
Asn	Tyr	Glu	Arg	Ala	Arg	Arg	Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	
		355					360					365				
Gly	Leu	Asp	Asp	Ile	His	Arg	Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	
	370					375					380					
Arg	Ala	Gln	Asp	Pro	Pro	Pro	Glu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	
385					390					395					400	

Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala
 405 410 415
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 420 425 430
 Val Gln Lys Ala Ala His Gly Val Arg Lys Ala Phe Lys Ser His Val
 435 440 445
 Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His
 450 455 460
 Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser
 465 470 475 480
 Ser Ser Leu Asn Glu Ala Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 485 490 495
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 500 505 510
 Gln Gly Ile
 515

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 514 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	130	135	140
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	145	150	155
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	165	170	175
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	180	185	190
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	195	200	205
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	210	215	220
Gly	Ser	Arg	Arg	Ala	Ser	Val	Gly	Ser	Val	Thr	Lys	Ala	Thr	Ser	Leu	225	230	235
Glu	Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	245	250	255
Gln	His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	260	265	270
Asp	Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	275	280	285
Ser	Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	290	295	300
Leu	Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	305	310	315
Leu	Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	325	330	335
Leu	Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	340	345	350
Gly	Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	355	360	365
Pro	Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	370	375	380
Lys	Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	385	390	395
Arg	Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	405	410	415
Tyr	Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	420	425	430
Trp	Gly	Ser	Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	435	440	445

Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr
 450 455 460
 Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly
 465 470 475 480
 Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu
 485 490 495
 Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
 500 505 510
 Arg Ser

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr		
			180					185					190				
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala		
		195					200					205					
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg		
	210					215					220						
Gly	Ser	Arg	Arg	Ala	Ser	Val	Gly	Ser	Val	Thr	Lys	Met	Pro	Arg	Ala		
225					230					235					240		
Pro	Arg	Cys	Arg	Ala	Val	Arg	Ser	Leu	Leu	Ser	His	Tyr	Arg	Glu	Val		
				245					250					255			
Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	Pro	Gln	Gly	Trp	Arg		
			260					265					270				
Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	Ala	Leu	Val	Ala	Gln		
		275					280					285					
Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	Pro	Ala	Ala	Pro	Ser		
	290					295					300						
Phe	Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu	Val	Ala	Arg	Val	Leu	Gln		
305					310					315					320		
Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala		
				325					330					335			
Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	Glu	Ala	Thr	Thr	Ser	Val		
			340					345					350				
Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly		
		355					360					365					
Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His		
	370					375					380						
Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	Leu	Val	Ala	Pro	Cys	Ala	Tyr		
385					390					395					400		
Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala		
				405					410					415			
Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu		
			420					425					430				
Arg	Ala	Trp	Asn	His	Ser	Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu		
		435					440					445					
Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu		
	450					455					460						
Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg		
465					470					475					480		
Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly		
				485					490					495			

Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu
500 505 510

Glu Ala Thr Ser Leu
515

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CCGGCCACCC CCCATATGCC GCGCGCTCCC 30

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

TGCGCACGTG GGAAGCCCTG GCAGATCTGA ATTCCACCAT GCCGCGCGCT CCCCCTG 58

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CGGGACGGGC TGCTCCTGCG TTTGGTGGAC GCGTTCTTGT TGGTGACACC TCACCTCACC 60

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Xaa	Xaa	Xaa	Arg	Xaa	Xaa	Pro	Lys	Xaa	Xaa	Xaa
1				5					10	

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1154 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Met	Pro	Arg	Ala	Pro	Arg	Cys	Arg	Ala	Val	Arg	Ser	Leu	Leu	Arg	Ser
1				5					10					15	
His	Tyr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly
			20					25						30	
Pro	Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg
		35					40					45			
Ala	Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro
	50					55					60				
Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu
65					70					75				80	
Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val
			85						90					95	
Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro
			100					105						110	
Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr
		115					120					125			
Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val
	130					135					140				
Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val
145					150					155				160	

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480

Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser		
				485					490						495		
Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met		
			500					505					510				
Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys		
		515					520					525					
Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe		
	530					535					540						
Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe		
545					550					555					560		
Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr		
				565					570					575			
Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His		
			580					585					590				
Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln		
		595					600					605					
His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile		
	610					615					620						
Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val		
625					630					635					640		
Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser		
				645				650						655			
Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala	Arg	Arg		
			660					665					670				
Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg		
		675					680					685					
Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro		
	690					695					700						
Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp	Thr	Ile		
705					710					715					720		
Pro	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	Pro	Gln		
				725					730					735			
Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	His		
			740					745					750				
Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu	Thr	Asp		
		755					760					765					
Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu	Thr	Ser		
	770					775						780					
Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu	Asn	Glu		
785					790					795					800		

Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815
 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910
 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
 915 920 925
 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
 930 935 940
 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
 945 950 955 960
 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
 965 970 975
 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
 980 985 990
 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
 995 1000 1005
 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
 1010 1015 1020
 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
 1025 1030 1035 1040
 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
 1045 1050 1055
 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
 1060 1065 1070
 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
 1075 1080 1085
 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
 1090 1095 1100
 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
 1105 1110 1115 1120

Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp Leu Glu Gln Lys
1125 1130 1135

Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His
1140 1145 1150

His His

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1200 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Met Pro Arg Gly Ser His His His His His His Gly Met Ala Ser Met
1 5 10 15

Thr Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Leu
20 25 30

Asp Pro Ser Ser Arg Ser Ala Ala Gly Thr Met Glu Phe Ala Ala Ala
35 40 45

Ser Thr Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu Ala Pro
50 55 60

Ala Thr Pro Ala Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser
65 70 75 80

Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val
85 90 95

Arg Arg Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro
100 105 110

Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp
115 120 125

Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys
130 135 140

Leu Lys Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly
145 150 155 160

Ala Lys Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg
165 170 175

Gly Gly Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro
180 185 190

Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu
195 200 205

Leu Arg Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys
 210 215 220
 Ala Leu Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly
 225 230 235 240
 Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro
 245 250 255
 His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn
 260 265 270
 His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly
 275 280 285
 Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys
 290 295 300
 Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly
 305 310 315 320
 Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg
 325 330 335
 Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser
 340 345 350
 Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly
 355 360 365
 Arg Gln His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro
 370 375 380
 Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu
 385 390 395 400
 Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser
 405 410 415
 Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile
 420 425 430
 Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro
 435 440 445
 Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu
 450 455 460
 Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His
 465 470 475 480
 Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg
 485 490 495
 Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp
 500 505 510
 Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln
 515 520 525

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Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
 850 855 860
 Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 865 870 875 880
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 885 890 895
 Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
 900 905 910
 Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
 915 920 925
 Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
 930 935 940
 Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro
 945 950 955 960
 Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
 965 970 975
 Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
 980 985 990
 His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
 995 1000 1005
 Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala
 1010 1015 1020
 Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg
 1025 1030 1035 1040
 Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp
 1045 1050 1055
 Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile
 1060 1065 1070
 Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro
 1075 1080 1085
 Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile
 1090 1095 1100
 Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala
 1105 1110 1115 1120
 Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu
 1125 1130 1135
 Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg
 1140 1145 1150
 His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln
 1155 1160 1165

Thr	Gln	Leu	Ser	Arg	Lys	Leu	Pro	Gly	Thr	Thr	Leu	Thr	Ala	Leu	Glu
1170						1175					1180				
Ala	Ala	Ala	Asn	Pro	Ala	Leu	Pro	Ser	Asp	Phe	Lys	Thr	Ile	Leu	Asp
1185					1190					1195					1200

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1189 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met	Lys	Phe	Leu	Val	Asn	Val	Ala	Leu	Val	Phe	Met	Val	Val	Tyr	Ile
1				5					10					15	
Ser	Tyr	Ile	Tyr	Ala	Asp	Pro	Ser	Ser	Arg	Ser	Ala	Ala	Gly	Thr	Met
			20					25					30		
Glu	Phe	Ala	Ala	Ala	Ser	Thr	Gln	Arg	Cys	Val	Leu	Leu	Arg	Thr	Trp
		35					40					45			
Glu	Ala	Leu	Ala	Pro	Ala	Thr	Pro	Ala	Met	Pro	Arg	Ala	Pro	Arg	Cys
	50					55					60				
Arg	Ala	Val	Arg	Ser	Leu	Leu	Arg	Ser	His	Tyr	Arg	Glu	Val	Leu	Pro
65					70					75					80
Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	Pro	Gln	Gly	Trp	Arg	Leu	Val
				85					90					95	
Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	Ala	Leu	Val	Ala	Gln	Cys	Leu
			100					105					110		
Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	Pro	Pro	Ala	Ala	Pro	Ser	Phe
		115					120					125			
Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg
	130					135					140				
Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu
145					150					155					160
Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val
				165					170					175	
Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly
			180					185					190		
Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His
		195					200					205			
Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala
	210					215					220				

Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln
225 230 235 240
Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys
245 250 255
Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly
260 265 270
Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser
275 280 285
Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu
290 295 300
Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg
305 310 315 320
Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala
325 330 335
Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser
340 345 350
His Pro Ser Val Gly Arg Gln His His Ala Gly Pro Pro Ser Thr Ser
355 360 365
Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu
370 375 380
Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro
385 390 395 400
Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg
405 410 415
Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr
420 425 430
Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro
435 440 445
Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val
450 455 460
Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala
465 470 475 480
Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu
485 490 495
Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His
500 505 510
Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg
515 520 525
Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe
530 535 540

Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu
 545 550 555 560
 Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp
 565 570 575
 Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg
 580 585 590
 Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val
 595 600 605
 Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr
 610 615 620
 Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys
 625 630 635 640
 Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg
 645 650 655
 Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala
 660 665 670
 Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg
 675 680 685
 Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg
 690 695 700
 Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser
 705 710 715 720
 Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser
 725 730 735
 Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu
 740 745 750
 Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val
 755 760 765
 Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu
 770 775 780
 Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg
 785 790 795 800
 Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe
 805 810 815
 Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln
 820 825 830
 Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val
 835 840 845
 Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp
 850 855 860

Val	Phe	Leu	Arg	Phe	Met	Cys	His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	
865					870					875					880	
Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	
				885					890					895		
Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly	Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	
			900					905					910			
Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	
		915					920					925				
Leu	Val	Thr	Pro	His	Leu	Thr	His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	
	930					935					940					
Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	
945					950					955					960	
Val	Val	Asn	Phe	Pro	Val	Glu	Asp	Glu	Ala	Leu	Gly	Gly	Thr	Ala	Phe	
				965					970					975		
Val	Gln	Met	Pro	Ala	His	Gly	Leu	Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu	
			980					985					990			
Asp	Thr	Arg	Thr	Leu	Glu	Val	Gln	Ser	Asp	Tyr	Ser	Ser	Tyr	Ala	Arg	
		995					1000					1005				
Thr	Ser	Ile	Arg	Ala	Ser	Leu	Thr	Phe	Asn	Arg	Gly	Phe	Lys	Ala	Gly	
	1010					1015					1020					
Arg	Asn	Met	Arg	Arg	Lys	Leu	Phe	Gly	Val	Leu	Arg	Leu	Lys	Cys	His	
1025					1030					1035					1040	
Ser	Leu	Phe	Leu	Asp	Leu	Gln	Val	Asn	Ser	Leu	Gln	Thr	Val	Cys	Thr	
				1045					1050					1055		
Asn	Ile	Tyr	Lys	Ile	Leu	Leu	Leu	Gln	Ala	Tyr	Arg	Phe	His	Ala	Cys	
			1060					1065					1070			
Val	Leu	Gln	Leu	Pro	Phe	His	Gln	Gln	Val	Trp	Lys	Asn	Pro	Thr	Phe	
		1075					1080					1085				
Phe	Leu	Arg	Val	Ile	Ser	Asp	Thr	Ala	Ser	Leu	Cys	Tyr	Ser	Ile	Leu	
	1090					1095					1100					
Lys	Ala	Lys	Asn	Ala	Gly	Met	Ser	Leu	Gly	Ala	Lys	Gly	Ala	Ala	Gly	
1105					1110					1115					1120	
Pro	Leu	Pro	Ser	Glu	Ala	Val	Gln	Trp	Leu	Cys	His	Gln	Ala	Phe	Leu	
				1125					1130					1135		
Leu	Lys	Leu	Thr	Arg	His	Arg	Val	Thr	Tyr	Val	Pro	Leu	Leu	Gly	Ser	
			1140					1145					1150			
Leu	Arg	Thr	Ala	Gln	Thr	Gln	Leu	Ser	Arg	Lys	Leu	Pro	Gly	Thr	Thr	
		1155					1160					1165				
Leu	Thr	Ala	Leu	Glu	Ala	Ala	Ala	Asn	Pro	Ala	Leu	Pro	Ser	Asp	Phe	
	1170					1175					1180					

Lys Thr Ile Leu Asp
1185

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Xaa Arg Xaa Ile Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Tyr Asp Xaa
1 5 10 15

Xaa

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 92 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

CTGCCCTCAG ACTTCAAGAC CATCCTGGAC TACAAGGACG ACGATGACAA ATGAATTCAG 60
ATCTGCGGCC GCCACCGCGG TGGAGCTCCA GC 92

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Tyr	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Gln	Gly	Xaa	Xaa	Xaa	Ser	Xaa	Xaa
1				5					10					15	
Xaa Xaa Xaa Xaa Xaa Xaa															
20															

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Asp	Xaa	Leu	Xaa	Xaa	Xaa
1				5					10			

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TTYTTYTAYG TNACNGA

17

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:
TCNGTNACRT ARAARAA 17

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:
MGNTTYATHC CNAARCC 17

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:
GCCACCCCCG CGCTGCCTCG AGCTCCCCGC TGC 33

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:
Pro Gln Asn Pro Lys Thr Pro Lys Pro Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Lys Lys Lys Lys Leu Arg
1 5

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Phe Arg Asn Lys Ile Leu Phe Pro His Lys Trp Arg Trp Ile Leu Ile
1 5 10 15

Trp Met Ile

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Lys Ile Tyr Phe Leu Ile His Ser Thr Ser Ile Ala Ala Leu Val Val
1 5 10 15

Thr Arg Lys Asp Ala Lys His Cys Asn Leu Ala Arg Asn Arg Leu His
 20 25 30

Cys Leu Phe Gln Ser Cys Lys Asn Asn
 35 40

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Ser	Ser	Thr	Ser	Arg	Met	Gln	Ile	Phe	Ile	Thr	Ile	Leu	Ser	Cys	Glu
1				5					10					15	

Asn

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Lys	Ala	Glu	Ser	Lys	Glu
1				5	

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Lys	Leu	Lys	His	Tyr
1			5	

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Cys Leu Asn Lys Ile Arg
1 5

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Cys Gly Leu Phe Tyr Phe Leu Asp His Phe Leu Arg Ser Ile Met Glu
1 5 10 15
Lys Ile Thr

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Lys Val Asn Ser Leu Asp Tyr Phe Pro Ser Gln Gln Cys Cys Val Tyr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Ile His Met Arg Met Ser Gln Arg Ile Ser Ile His Gln Thr Tyr Gln
1 5 10 15

Arg Gln Thr Arg Tyr Lys Thr Gln Glu Lys Val Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Ser Asn Ser Arg Arg Thr Tyr Cys Ile Tyr Tyr Ser Tyr Gly Phe Tyr
 1 5 10 15
 Tyr Asn Cys Phe Arg Tyr Arg Arg Cys Thr Pro Glu Ser Cys Asp Asn
 20 25 30
 Cys Lys Ser Cys Leu Gln Leu Lys Glu Ser Gln Phe Cys Lys Phe Cys
 35 40 45
 Cys Val Cys His Tyr Phe Val Asn
 50 55

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ser Gln Ile Ser Tyr Leu Asn Leu Met Asp Ser Tyr Arg Asn Lys Pro
 1 5 10 15
 Asn Lys Pro Cys Lys Phe Asn Gly Ile Tyr Val Lys Ser Phe Gly Thr
 20 25 30
 Asn Ala His Cys Ile Tyr Ile Gly Phe Leu Lys His Arg Tyr Thr Glu
 35 40 45
 Cys Phe Arg Asp Cys Phe Ser Leu Gln Gln Ile Thr Cys Phe Asp Tyr
 50 55 60
 Ser Cys Ser Ser Leu Ile Ser Leu Lys Glu Ala Gly Glu Met Lys Arg
 65 70 75 80
 Arg Leu Lys Lys Glu Ile Ser Lys Phe Val Asp Ser Ser Val Thr Gly
 85 90 95

Ile Asn Asn Lys Asn Ile Ser Asn Glu Lys Glu Glu Glu Leu Ser Gln
100 105 110

Ser Cys Phe Leu Lys Ile Ser Lys Ile Pro Gly Lys Arg Asp Thr Phe
115 120 125

Ile Lys Ile His Ile Leu
130

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Phe Phe Ile Ser Gln Leu Leu Phe Ser Phe Ile Leu Thr Ile Phe Phe
1 5 10 15

Asp

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Leu Glu Val Lys Ser Ile Lys
1 5

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Thr Glu Val Thr
1

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Leu	Ile	His	Ile	His	Arg	Ser	Thr	Phe	Ile	Tyr	Pro	Ile	Arg	Cys
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Gly	Asn	Ser	Ser	His	Pro	Phe
1				5		

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Cys	Tyr	Glu	Asp
1			

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

```
Ile Phe Arg Val Lys Lys Trp Ser Arg Asn Leu Asn Gln Lys Glu Leu
1           5           10           15

Arg Arg Tyr Cys Lys Arg Ile Glu Leu
          20           25
```

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```
Val Leu Pro Ile Leu Ile Asp Cys Arg Asp Cys Arg Gly Asn Cys Thr
1           5           10           15

Glu Asp His
```

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```
Arg Asn Lys Val Thr Phe Ile Asn
1           5
```

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```
Ile Thr Asn Ile Glu Ile Ser Asp Leu Gln Leu Thr Lys
1           5           10
```

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Thr	Ile	Lys	Asn	Thr	Asn	Leu	Gly	Gln	Asn	Ile	Glu	Glu	Gly	Lys	Glu
1				5					10					15	
Asp	Gln	Leu	Ala	Lys	Glu	Lys	Ile	Arg	Gln						
		20						25							

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Ile	Lys	Cys	Val	Gln	Lys	Cys	Arg	Asn	Lys	Arg	Phe	Ile	Phe	Phe	Asn
1				5					10					15	
Asn	Leu	Leu	Lys	Arg	Gly	Val	Leu	Gly	Phe	Trp	Gly	Phe	Gly		
		20						25					30		

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

Pro	Lys	Thr	Pro	Lys	Pro	Gln	Asn	Pro	Tyr	Lys	Lys	Arg	Lys	Asn	Cys
1				5					10					15	
Gly	Ser	Leu	Glu	Ile	Lys	Tyr	Tyr	Ser	Arg	Thr	Asn	Gly	Asp	Gly	Tyr
		20						25					30		
Cys	Phe	Gly	Cys	Tyr	Arg	Lys	Phe	Thr	Ser						
		35					40								

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Tyr Ile Gln Gln Val
1 5

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Cys Gln Glu Arg Met Gln Asn Ile Glu Ile Trp Leu Glu Ile Ala Phe
1 5 10 15
Ile Asp Tyr Ser Lys Val Ala Lys Thr Ile Arg Val Leu Leu Leu Gly
20 25 30
Cys Lys Ser Leu
35

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Arg Phe Phe Leu Glu Lys Ile Ser Phe Lys Lys Arg Arg Ala Lys Ser
1 5 10 15
Arg Asn Cys Asn Ile Thr Asn Val
20

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Ile Lys Ser Gly Asn Glu Asp Tyr Ser Ile Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Gly Ala Leu Trp Arg Lys Leu Leu Asn Thr Lys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Thr Val Trp Ile Ile Ser Leu Ala Asn Asn Asp Glu Tyr Ile Lys Phe
1 5 10 15

Ile Cys Glu Cys Val Lys Gly Ser Arg Tyr Ile Arg Leu Thr Lys Asp
20 25 30

Lys Leu Ala Ile Lys Arg Lys Lys Lys Phe Asp Asn Arg Thr Ala Glu
35 40 45

Glu Leu Ile Ala Phe Thr Ile Arg Met Gly Phe Ile Thr Ile Val Leu
50 55 60

Gly Ile Asp Gly Glu Leu Pro Ser Leu Glu Thr Ile Glu Lys Ala Val
65 70 75 80

Tyr Asn Cys Arg Asn Arg Ser Ser Glu Ser Ser Asp Val Tyr Ala Ile
85 90 95

Ile Leu Cys Ile Asn Leu Lys Tyr Leu Ile Ser Ile
100 105

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Trp Ile Ala Ile Glu Thr Asn Gln Ile Asn His Ala Ser Leu Met Glu
1 5 10 15

Tyr Thr Leu Asn Pro Leu Gly Gln Met His Thr Glu Phe Ile Leu Asp
20 25 30

Ser

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Ser Ile Asp Thr Gln Asn Ala Leu Glu Thr Asp Leu Ala Tyr Asn Arg
1 5 10 15

Leu Pro Val Leu Ile Thr Leu Ala His Leu Leu Tyr Leu
20 25

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Lys Lys Gln Ala Lys Cys Lys Glu Asp
1 5

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Arg Lys Arg Phe Gln Asn Leu Leu Ile Leu Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Pro Glu Leu Thr Thr Arg Ile Leu Ala Thr Lys Lys Lys Lys Ser Tyr
1 5 10 15
His Asn Pro Asp Ser
20

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Arg Phe Gln Lys Phe Gln Val Arg Glu Ile His Ser Leu Lys Phe Ile
1 5 10 15
Tyr Tyr Ser Phe Ser Phe His Ser Cys Tyr Phe Leu Leu Ser
20 25 30

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Gln Tyr Phe Leu Ile Ser Trp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Lys Val Ser Asn Lys Arg Ser Ala Arg Leu Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Leu Ser Leu Phe Thr Phe Ile Asp Arg Pro Ser Tyr Ile Gln Tyr Asp
1 5 10 15

Asp Lys Glu Thr Ala Val Ile Arg Phe Lys Asn Ser Ala Met Arg Thr
 20 25 30

Lys Phe Leu Glu Ser Arg Asn Gly Ala Glu Ile Leu Ile Lys Lys Asn
 35 40 45

Cys Val Asp Ile Ala Lys Glu Ser Asn Ser Lys Ser Phe Val Asn Lys
 50 55 60

Tyr Tyr Gln Ser Cys Leu Ile Glu Glu Ile Asp Glu Ala Thr Ala Gln
65 70 75 80

Lys Ile Ile Lys Glu Ile Lys
85

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Leu Leu Leu Ile Arg Glu
1 5

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Thr Lys Leu Leu Ile
1 5

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Arg Ser Ala Ile Phe Asn Cys Arg Asn Lys Ser Cys Thr Lys Val Arg
1 5 10 15
Gln

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Lys	Ile	Gln	Thr	Leu	Val	Lys	Ile	Leu	Arg	Lys	Glu	Lys	Lys	Thr	Ser
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Gln	Lys	Lys	Lys
1			

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Asn	Glu	Tyr	Arg	Ser	Glu	Glu	Ile	Lys	Asp	Leu	Phe	Phe	Ser	Ile	Ile
1				5				10						15	
Tyr	Cys	Lys	Glu	Gly	Phe	Trp	Gly	Phe	Gly	Val	Leu	Gly			
			20				25								

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Pro Lys Pro Gln Asn Pro Lys Thr Pro Ile Lys Lys Glu Lys Ile Glu
1 5 10 15
Val Val

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Asn Ile Ile Pro Ala Gln Met Glu Met Asp Ile Asp Leu Asp Asp Ile
1 5 10 15
Glu Asn Leu Leu Pro Asn Thr Phe Asn Lys Tyr Ser Ser Ser Cys Ser
20 25 30
Asp Lys Lys Gly Cys Lys Thr Leu Lys Ser Gly Ser Lys Ser Pro Ser
35 40 45
Leu Thr Ile Pro Lys Leu Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp
50 55 60
Ala Asn Leu Tyr Asn Asp Ser Phe Leu Arg Lys Leu Val Leu Lys Ser
65 70 75 80
Gly Glu Gln Arg Val Glu Ile Glu Thr Leu Leu Met Phe Lys
85 90

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Asn Gln Val Met Arg Ile Ile Leu Phe Phe Arg Ser Leu Leu Lys Glu
1 5 10 15

His Tyr Gly Glu Asn Tyr Leu Ile Leu Lys Gly Lys Gln Phe Gly Leu
 20 25 30
 Phe Pro

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Pro Thr Met Met Ser Ile Leu Asn Ser Tyr Glu Asn Glu Ser Lys Asp
 1 5 10 15
 Leu Asp Thr Ser Asp Leu Pro Lys Thr Asn Ser Leu
 20 25

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Asn Ala Arg Lys Ser Leu Ile Ile Glu Gln Gln Lys Asn Leu Leu His
 1 5 10 15
 Leu Leu Phe Val Trp Val Leu Leu Gln Leu Phe
 20 25

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Val Ser Thr Val Asn Ser Arg Val Leu Arg Gln Leu Lys Lys Leu Phe
 1 5 10 15

Thr	Thr	Glu	Gly	Ile	Ala	Val	Leu	Lys	Val	Leu	Met	Cys	Met	Pro	Leu
			20					25					30		
Phe	Cys	Glu	Leu	Ile	Ser	Asn	Ile	Leu	Ser	Gln	Phe	Asn	Gly		
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Lys Gln Thr Lys
1

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Thr Met Gln Val
1

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Trp Asn Ile Arg
1

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Ile	Leu	Trp	Asp	Lys	Cys	Thr	Leu	Asn	Leu	Tyr	Trp	Ile	Leu	Lys	Ala
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Ile	His	Arg	Met	Leu
1				5

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Leu	Thr	Thr	Asp	Tyr	Leu	Phe	Cys	Leu	Leu	Leu	Leu	Ile	Ser	Tyr	Ile
1				5				10						15	
Phe	Lys	Arg	Ser	Arg	Arg	Asn	Glu	Lys	Lys	Thr	Lys	Glu	Arg	Asp	Phe
			20					25					30		
Lys	Ile	Cys	Cys	Phe	Phe	Cys	Asn	Arg	Asn						
		35					40								

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Gln Gln Glu Tyr
1

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Gln Arg Lys Arg Arg Arg Ala Ile Thr Ile Leu Ile Leu Lys Asp Phe
1 5 10 15

Lys Asn Ser Arg
20

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Glu Arg Tyr Ile His
1 5

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Asn Ser Tyr Ile Ile Val Phe His Phe Thr Ala Val Ile Phe Phe Tyr
1 5 10 15
Leu Asn Asn Ile Phe Cys Leu Ala Gly Ser Lys Lys Tyr Gln Ile Arg
 20 25 30
Glu Ala Leu Asp Cys Gly Asn Leu Ala Tyr Ser His Ser
 35 40 45

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

Ile Asp Leu His Ile Ser Asn Thr Met Ile Arg Lys Gln Gln Ser Ser
1 5 10 15
Val Leu Lys Ile Val Leu Cys Gly Leu Asn Phe
 20 25

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Ser Gln Glu Met Glu Pro Lys Ser
1 5

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Ser Lys Arg Ile Ala Ser Ile Leu Gln Lys Asn Arg Thr Leu Asn Leu
1 5 10 15
Ser Leu Ile Ser Ile Thr Asn Leu Asp Cys Leu Lys Arg Leu Thr Arg
20 25 30
Gln Leu His Arg Arg Ser Leu Lys Lys
35 40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Ser Asn Phe Tyr
1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Leu Glu Asn Lys Leu Asn Tyr
1 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Tyr Arg Asp Gln Arg Ser Ser Ile Asp Glu Ile Lys Ala Glu Leu Lys
1 5 10 15

Leu Asp Asn Lys Lys Tyr Lys Pro Trp Ser Lys Tyr Cys Gly Arg Lys
 20 25 30
 Arg Arg Pro Val Ser Lys Arg Lys Asn Lys Ala Ile Asn Lys Met Ser
 35 40 45
 Thr Glu Val Lys Lys
 50

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Lys Ile Tyr Phe Phe Gln
 1 5

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Phe Ile Glu Lys Arg Gly Phe Gly Val Leu Gly Phe Trp
 1 5 10

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1007 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser Ala
 1 5 10 15

Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser Trp
 20 25 30
 Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr Lys
 35 40 45
 Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala Thr
 50 55 60
 Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys Glu
 65 70 75 80
 Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu Val
 85 90 95
 Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln Cys
 100 105 110
 Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu Leu
 115 120 125
 Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp Asn
 130 135 140
 Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr Thr
 145 150 155 160
 Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln Phe
 165 170 175
 Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe Asp
 180 185 190
 Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys Cys
 195 200 205
 Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu Asn
 210 215 220
 Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg Ile
 225 230 235 240
 Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys His
 245 250 255
 Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala Gln
 260 265 270
 Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys Leu
 275 280 285
 Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val Lys
 290 295 300
 Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro Glu
 305 310 315 320
 Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys Thr
 325 330 335

Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr Thr
 340 345 350
 Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn Ile
 355 360 365
 Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln Lys
 370 375 380
 Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His Lys
 385 390 395 400
 Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met Gln
 405 410 415
 Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn Ile
 420 425 430
 Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val Val
 435 440 445
 Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr
 450 455 460
 Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys
 465 470 475 480
 Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu
 485 490 495
 Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys
 500 505 510
 Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe
 515 520 525
 Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr
 530 535 540
 Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn
 545 550 555 560
 Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp
 565 570 575
 Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly
 580 585 590
 Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp
 595 600 605
 Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys Leu
 610 615 620
 Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg Lys
 625 630 635 640
 Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met Lys
 645 650 655

Asp	Tyr	Phe	Arg	Gln	Lys	Phe	Gln	Lys	Ile	Ala	Leu	Glu	Gly	Gly	Gln		
			660					665					670				
Tyr	Pro	Thr	Leu	Phe	Ser	Val	Leu	Glu	Asn	Glu	Gln	Asn	Asp	Leu	Asn		
		675					680					685					
Ala	Lys	Lys	Thr	Leu	Ile	Val	Glu	Ala	Lys	Gln	Arg	Asn	Tyr	Phe	Lys		
	690					695					700						
Lys	Asp	Asn	Leu	Leu	Gln	Pro	Val	Ile	Asn	Ile	Cys	Gln	Tyr	Asn	Tyr		
705					710					715					720		
Ile	Asn	Phe	Asn	Gly	Lys	Phe	Tyr	Lys	Gln	Thr	Lys	Gly	Ile	Pro	Gln		
				725					730					735			
Gly	Leu	Cys	Val	Ser	Ser	Ile	Leu	Ser	Ser	Phe	Tyr	Tyr	Ala	Thr	Leu		
			740					745					750				
Glu	Glu	Ser	Ser	Leu	Gly	Phe	Leu	Arg	Asp	Glu	Ser	Met	Asn	Pro	Glu		
		755					760					765					
Asn	Pro	Asn	Val	Asn	Leu	Leu	Met	Arg	Leu	Thr	Asp	Asp	Tyr	Leu	Leu		
	770					775					780						
Ile	Thr	Thr	Gln	Glu	Asn	Asn	Ala	Val	Leu	Phe	Ile	Glu	Lys	Leu	Ile		
785					790					795					800		
Asn	Val	Ser	Arg	Glu	Asn	Gly	Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu	Gln		
				805					810					815			
Thr	Ser	Phe	Pro	Leu	Ser	Pro	Ser	Lys	Phe	Ala	Lys	Tyr	Gly	Met	Asp		
			820					825					830				
Ser	Val	Glu	Glu	Gln	Asn	Ile	Val	Gln	Asp	Tyr	Cys	Asp	Trp	Ile	Gly		
		835					840					845					
Ile	Ser	Ile	Asp	Met	Lys	Thr	Leu	Ala	Leu	Met	Pro	Asn	Ile	Asn	Leu		
	850					855					860						
Arg	Ile	Glu	Gly	Ile	Leu	Cys	Thr	Leu	Asn	Leu	Asn	Met	Gln	Thr	Lys		
865					870					875					880		
Lys	Ala	Ser	Met	Trp	Leu	Lys	Lys	Lys	Leu	Lys	Ser	Phe	Leu	Met	Asn		
				885					890					895			
Asn	Ile	Thr	His	Tyr	Phe	Arg	Lys	Thr	Ile	Thr	Thr	Glu	Asp	Phe	Ala		
			900					905					910				
Asn	Lys	Thr	Leu	Asn	Lys	Leu	Phe	Ile	Ser	Gly	Gly	Tyr	Lys	Tyr	Met		
		915					920					925					
Gln	Cys	Ala	Lys	Glu	Tyr	Lys	Asp	His	Phe	Lys	Lys	Asn	Leu	Ala	Met		
	930					935						940					
Ser	Ser	Met	Ile	Asp	Leu	Glu	Val	Ser	Lys	Ile	Ile	Tyr	Ser	Val	Thr		
945					950					955					960		
Arg	Ala	Phe	Phe	Lys	Tyr	Leu	Val	Cys	Asn	Ile	Lys	Asp	Thr	Ile	Phe		
				965					970					975			

Gly	Glu	Glu	His	Tyr	Pro	Asp	Phe	Phe	Leu	Ser	Thr	Leu	Lys	His	Phe
			980					985					990		
Ile	Glu	Ile	Phe	Ser	Thr	Lys	Lys	Tyr	Ile	Phe	Asn	Arg	Val	Cys	
			995				1000					1005			

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 699 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Glu	Leu	Glu	Leu	Glu	Met	Gln	Glu	Asn	Gln	Asn	Asp	Ile	Gln	Val	Arg
1				5				10					15		
Val	Lys	Ile	Asp	Asp	Pro	Lys	Gln	Tyr	Leu	Val	Asn	Val	Thr	Ala	Ala
			20					25					30		
Cys	Leu	Leu	Gln	Glu	Gly	Ser	Tyr	Tyr	Gln	Asp	Lys	Asp	Glu	Arg	Arg
			35				40					45			
Tyr	Ile	Ile	Thr	Lys	Ala	Leu	Leu	Glu	Val	Ala	Glu	Ser	Asp	Pro	Glu
	50					55					60				
Phe	Ile	Cys	Gln	Leu	Ala	Val	Tyr	Ile	Arg	Asn	Glu	Leu	Tyr	Ile	Arg
65					70					75					80
Thr	Thr	Thr	Asn	Tyr	Ile	Val	Ala	Phe	Cys	Val	Val	His	Lys	Asn	Thr
			85						90					95	
Gln	Pro	Phe	Ile	Glu	Lys	Tyr	Phe	Asn	Lys	Ala	Val	Leu	Leu	Pro	Asn
			100					105					110		
Asp	Leu	Leu	Glu	Val	Cys	Glu	Phe	Ala	Gln	Val	Leu	Tyr	Ile	Phe	Asp
			115				120					125			
Ala	Thr	Glu	Phe	Lys	Asn	Leu	Tyr	Leu	Asp	Arg	Ile	Leu	Ser	Gln	Asp
			130			135					140				
Ile	Arg	Lys	Glu	Leu	Thr	Phe	Arg	Lys	Cys	Leu	Gln	Arg	Cys	Val	Arg
145					150					155					160
Ser	Lys	Phe	Ser	Glu	Phe	Asn	Glu	Tyr	Gln	Leu	Gly	Lys	Tyr	Cys	Thr
				165					170					175	
Glu	Ser	Gln	Arg	Lys	Lys	Thr	Met	Phe	Arg	Tyr	Leu	Ser	Val	Thr	Asn
			180					185					190		
Lys	Gln	Lys	Trp	Asp	Gln	Thr	Lys	Lys	Lys	Arg	Lys	Glu	Asn	Leu	Leu
			195				200					205			
Thr	Lys	Leu	Gln	Ala	Ile	Lys	Glu	Ser	Glu	Asp	Lys	Ser	Lys	Arg	Glu
			210			215					220				

Thr	Gly	Asp	Ile	Met	Asn	Val	Glu	Asp	Ala	Ile	Lys	Ala	Leu	Lys	Pro	225	230	235	240
Ala	Val	Met	Lys	Lys	Ile	Ala	Lys	Arg	Gln	Asn	Ala	Met	Lys	Lys	His	245	250	255	
Met	Lys	Ala	Pro	Lys	Ile	Pro	Asn	Ser	Thr	Leu	Glu	Ser	Lys	Tyr	Leu	260	265	270	
Thr	Phe	Lys	Asp	Leu	Ile	Lys	Phe	Cys	His	Ile	Ser	Glu	Pro	Lys	Glu	275	280	285	
Arg	Val	Tyr	Lys	Ile	Leu	Gly	Lys	Lys	Tyr	Pro	Lys	Thr	Glu	Glu	Glu	290	295	300	
Tyr	Lys	Ala	Ala	Phe	Gly	Asp	Ser	Ala	Ser	Ala	Pro	Phe	Asn	Pro	Glu	305	310	315	320
Leu	Ala	Gly	Lys	Arg	Met	Lys	Ile	Glu	Ile	Ser	Lys	Thr	Trp	Glu	Asn	325	330	335	
Glu	Leu	Ser	Ala	Lys	Gly	Asn	Thr	Ala	Glu	Val	Trp	Asp	Asn	Leu	Ile	340	345	350	
Ser	Ser	Asn	Gln	Leu	Pro	Tyr	Met	Ala	Met	Leu	Arg	Asn	Leu	Ser	Asn	355	360	365	
Ile	Leu	Lys	Ala	Gly	Val	Ser	Asp	Thr	Thr	His	Ser	Ile	Val	Ile	Asn	370	375	380	
Lys	Ile	Cys	Glu	Pro	Lys	Ala	Val	Glu	Asn	Ser	Lys	Met	Phe	Pro	Leu	385	390	395	400
Gln	Phe	Phe	Ser	Ala	Ile	Glu	Ala	Val	Asn	Glu	Ala	Val	Thr	Lys	Gly	405	410	415	
Phe	Lys	Ala	Lys	Lys	Arg	Glu	Asn	Met	Asn	Leu	Lys	Gly	Gln	Ile	Glu	420	425	430	
Ala	Val	Lys	Glu	Val	Val	Glu	Lys	Thr	Asp	Glu	Glu	Lys	Lys	Asp	Met	435	440	445	
Glu	Leu	Glu	Gln	Thr	Glu	Glu	Gly	Glu	Phe	Val	Lys	Val	Asn	Glu	Gly	450	455	460	
Ile	Gly	Lys	Gln	Tyr	Ile	Asn	Ser	Ile	Glu	Leu	Ala	Ile	Lys	Ile	Ala	465	470	475	480
Val	Asn	Lys	Asn	Leu	Asp	Glu	Ile	Lys	Gly	His	Thr	Ala	Ile	Phe	Ser	485	490	495	
Asp	Val	Ser	Gly	Ser	Met	Ser	Thr	Ser	Met	Ser	Gly	Gly	Ala	Lys	Lys	500	505	510	
Tyr	Gly	Ser	Val	Arg	Thr	Cys	Leu	Glu	Cys	Ala	Leu	Val	Leu	Gly	Leu	515	520	525	
Met	Val	Lys	Gln	Arg	Cys	Glu	Lys	Ser	Ser	Phe	Tyr	Ile	Phe	Ser	Ser	530	535	540	

Pro	Ser	Ser	Gln	Cys	Asn	Lys	Cys	Tyr	Leu	Glu	Val	Asp	Leu	Pro	Gly	545	550	555	560
Asp	Glu	Leu	Arg	Pro	Ser	Met	Gln	Lys	Leu	Leu	Gln	Glu	Lys	Gly	Lys	565	570	575	
Leu	Gly	Gly	Gly	Thr	Asp	Phe	Pro	Tyr	Glu	Cys	Ile	Asp	Glu	Trp	Thr	580	585	590	
Lys	Asn	Lys	Thr	His	Val	Asp	Asn	Ile	Val	Ile	Leu	Ser	Asp	Met	Met	595	600	605	
Ile	Ala	Glu	Gly	Tyr	Ser	Asp	Ile	Asn	Val	Arg	Gly	Ser	Ser	Ile	Val	610	615	620	
Asn	Ser	Ile	Lys	Lys	Tyr	Lys	Asp	Glu	Val	Asn	Pro	Asn	Ile	Lys	Ile	625	630	635	640
Phe	Ala	Val	Asp	Leu	Glu	Gly	Tyr	Gly	Lys	Cys	Leu	Asn	Leu	Gly	Asp	645	650	655	
Glu	Phe	Asn	Glu	Asn	Asn	Tyr	Ile	Lys	Ile	Phe	Gly	Met	Ser	Asp	Ser	660	665	670	
Ile	Leu	Lys	Phe	Ile	Ser	Ala	Lys	Gln	Gly	Gly	Ala	Asn	Met	Val	Glu	675	680	685	
Val	Ile	Lys	Asn	Phe	Ala	Leu	Gln	Lys	Ile	Gly						690	695		

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Leu	Ser	Thr	Gln	Lys	Gln	Tyr	Phe	Phe	Gln	Asp	Glu	Trp	Asn	Gln	Val	1	5	10	15
Arg	Ala	Met	Ile	Gly	Asn	Glu	Leu	Phe	Arg	His	Leu	Tyr	Thr	Lys	Tyr	20	25	30	
Leu	Ile	Phe	Gln	Arg	Thr	Ser	Glu	Gly	Thr	Leu	Val	Gln	Phe	Cys	Gly	35	40	45	
Asn	Asn	Val	Phe	Asp	His	Leu	Lys	Val	Asn	Asp	Lys	Phe	Asp	Lys	Lys	50	55	60	
Gln	Lys	Gly	Gly	Ala	Ala	Asp	Met	Asn	Glu	Pro	Arg	Cys	Cys	Ser	Thr	65	70	75	80
Cys	Lys	Tyr	Asn	Val	Lys	Asn	Glu	Lys	Asp	His	Phe	Leu	Asn	Asn	Ile	85	90	95	

Asn	Val	Pro	Asn	Trp	Asn	Asn	Met	Lys	Ser	Arg	Thr	Arg	Ile	Phe	Tyr		
			100					105					110				
Cys	Thr	His	Phe	Asn	Arg	Asn	Asn	Gln	Phe	Phe	Lys	Lys	His	Glu	Phe		
		115					120					125					
Val	Ser	Asn	Lys	Asn	Asn	Ile	Ser	Ala	Met	Asp	Arg	Ala	Gln	Thr	Ile		
	130					135					140						
Phe	Thr	Asn	Ile	Phe	Arg	Phe	Asn	Arg	Ile	Arg	Lys	Lys	Leu	Lys	Asp		
145					150					155					160		
Lys	Val	Ile	Glu	Lys	Ile	Ala	Tyr	Met	Leu	Glu	Lys	Val	Lys	Asp	Phe		
				165					170					175			
Asn	Phe	Asn	Tyr	Tyr	Leu	Thr	Lys	Ser	Cys	Pro	Leu	Pro	Glu	Asn	Trp		
			180					185					190				
Arg	Glu	Arg	Lys	Gln	Lys	Ile	Glu	Asn	Leu	Ile	Asn	Lys	Thr	Arg	Glu		
	195						200					205					
Glu	Lys	Ser	Lys	Tyr	Tyr	Glu	Glu	Leu	Phe	Ser	Tyr	Thr	Thr	Asp	Asn		
	210					215					220						
Lys	Cys	Val	Thr	Gln	Phe	Ile	Asn	Glu	Phe	Phe	Tyr	Asn	Ile	Leu	Pro		
225					230					235					240		
Lys	Asp	Phe	Leu	Thr	Gly	Arg	Asn	Arg	Lys	Asn	Phe	Gln	Lys	Lys	Val		
				245					250					255			
Lys	Lys	Tyr	Val	Glu	Leu	Asn	Lys	His	Glu	Leu	Ile	His	Lys	Asn	Leu		
			260					265					270				
Leu	Leu	Glu	Lys	Ile	Asn	Thr	Arg	Glu	Ile	Ser	Trp	Met	Gln	Val	Glu		
		275					280					285					
Thr	Ser	Ala	Lys	His	Phe	Tyr	Tyr	Phe	Asp	His	Glu	Asn	Ile	Tyr	Val		
	290					295					300						
Leu	Trp	Lys	Leu	Leu	Arg	Trp	Ile	Phe	Glu	Asp	Leu	Val	Val	Ser	Leu		
305					310					315					320		
Ile	Arg	Cys	Phe	Phe	Tyr	Val	Thr	Glu	Gln	Gln	Lys	Ser	Tyr	Ser	Lys		
			325						330					335			
Thr	Tyr	Tyr	Tyr	Arg	Lys	Asn	Ile	Trp	Asp	Val	Ile	Met	Lys	Met	Ser		
			340					345					350				
Ile	Ala	Asp	Leu	Lys	Lys	Glu	Thr	Leu	Ala	Glu	Val	Gln	Glu	Lys	Glu		
		355					360					365					
Val	Glu	Glu	Trp	Lys	Lys	Ser	Leu	Gly	Phe	Ala	Pro	Gly	Lys	Leu	Arg		
	370					375					380						
Leu	Ile	Pro	Lys	Lys	Thr	Thr	Phe	Arg	Pro	Ile	Met	Thr	Phe	Asn	Lys		
385					390					395					400		
Lys	Ile	Val	Asn	Ser	Asp	Arg	Lys	Thr	Thr	Lys	Leu	Thr	Thr	Asn	Thr		
			405						410					415			

Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn Arg Met
 420 425 430
 Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp Val Met
 435 440 445
 Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly Gln Pro
 450 455 460
 Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser Val
 465 470 475 480
 Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys Leu Leu Ser
 485 490 495
 Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg Lys Asn Asn
 500 505 510
 Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met Lys Asp Tyr
 515 520 525
 Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly Gln Tyr Pro
 530 535 540
 Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu Asn Ala Lys
 545 550 555 560
 Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe Lys Lys Asp
 565 570 575
 Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn Tyr Ile Asn
 580 585 590
 Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu
 595 600 605
 Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu
 610 615 620
 Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn Pro
 625 630 635 640
 Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr
 645 650 655
 Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val
 660 665 670
 Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Ser
 675 680 685
 Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met Asp Ser Val
 690 695 700
 Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile Gly Ile Ser
 705 710 715 720
 Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn Leu Arg Ile
 725 730 735

Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr Lys Lys Ala
 740 745 750
 Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met Asn Asn Ile
 755 760 765
 Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe Ala Asn Lys
 770 775 780
 Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Met Gln Cys
 785 790 795 800
 Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala Met Ser Ser
 805 810 815
 Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Thr Arg Ala
 820 825 830
 Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile Phe Gly Glu
 835 840 845
 Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His Phe Ile Glu
 850 855 860
 Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys Met Ile Leu
 865 870 875 880
 Lys Ala Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln Ser Leu Ile
 885 890 895
 Gln

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 840 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Met Ser Arg Arg Asn Gln Lys Lys Pro Gln Ala Pro Ile Gly Asn Glu
 1 5 10 15
 Thr Asn Leu Asp Phe Val Leu Gln Asn Leu Glu Val Tyr Lys Ser Gln
 20 25 30
 Ile Glu His Tyr Lys Thr Gln Gln Gln Gln Ile Lys Glu Glu Asp Leu
 35 40 45
 Lys Leu Leu Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn
 50 55 60
 Asp Asp Asp Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu
 65 70 75 80

Arg	Arg	Val	Asn	Gln	Ile	Lys	Gln	Gln	Val	Gln	Leu	Ile	Lys	Lys	Val	85	90	95
Gly	Ser	Lys	Val	Glu	Lys	Asp	Leu	Asn	Leu	Asn	Glu	Asp	Glu	Asn	Lys	100	105	110
Lys	Asn	Gly	Leu	Ser	Glu	Gln	Gln	Val	Lys	Glu	Glu	Gln	Leu	Arg	Thr	115	120	125
Ile	Thr	Glu	Glu	Gln	Val	Lys	Tyr	Gln	Asn	Leu	Val	Phe	Asn	Met	Asp	130	135	140
Tyr	Gln	Leu	Asp	Leu	Asn	Glu	Ser	Gly	Gly	His	Arg	Arg	His	Arg	Arg	145	150	155
Glu	Thr	Asp	Tyr	Asp	Thr	Glu	Lys	Trp	Phe	Glu	Ile	Ser	His	Asp	Gln	165	170	175
Lys	Asn	Tyr	Val	Ser	Ile	Tyr	Ala	Asn	Gln	Lys	Thr	Ser	Tyr	Cys	Trp	180	185	190
Trp	Leu	Lys	Asp	Tyr	Phe	Asn	Lys	Asn	Asn	Tyr	Asp	His	Leu	Asn	Val	195	200	205
Ser	Ile	Asn	Arg	Leu	Glu	Thr	Glu	Ala	Glu	Phe	Tyr	Ala	Phe	Asp	Asp	210	215	220
Phe	Ser	Gln	Thr	Ile	Lys	Leu	Thr	Asn	Asn	Ser	Tyr	Gln	Thr	Val	Asn	225	230	235
Ile	Asp	Val	Asn	Phe	Asp	Asn	Asn	Leu	Cys	Ile	Leu	Ala	Leu	Leu	Arg	245	250	255
Phe	Leu	Leu	Ser	Leu	Glu	Arg	Phe	Asn	Ile	Leu	Asn	Ile	Arg	Ser	Ser	260	265	270
Tyr	Thr	Arg	Asn	Gln	Tyr	Asn	Phe	Glu	Lys	Ile	Gly	Glu	Leu	Leu	Glu	275	280	285
Thr	Ile	Phe	Ala	Val	Val	Phe	Ser	His	Arg	His	Leu	Gln	Gly	Ile	His	290	295	300
Leu	Gln	Val	Pro	Cys	Glu	Ala	Phe	Gln	Tyr	Leu	Val	Asn	Ser	Ser	Ser	305	310	315
Gln	Ile	Ser	Val	Lys	Asp	Ser	Gln	Leu	Gln	Val	Tyr	Ser	Phe	Ser	Thr	325	330	335
Asp	Leu	Lys	Leu	Val	Asp	Thr	Asn	Lys	Val	Gln	Asp	Tyr	Phe	Lys	Phe	340	345	350
Leu	Gln	Glu	Phe	Pro	Arg	Leu	Thr	His	Val	Ser	Gln	Gln	Ala	Ile	Pro	355	360	365
Val	Ser	Ala	Thr	Asn	Ala	Val	Glu	Asn	Leu	Asn	Val	Leu	Leu	Lys	Lys	370	375	380
Val	Lys	His	Ala	Asn	Leu	Asn	Leu	Val	Ser	Ile	Pro	Thr	Gln	Phe	Asn	385	390	395
																400		

Phe	Asp	Phe	Tyr	Phe	Val	Asn	Leu	Gln	His	Leu	Lys	Leu	Glu	Phe	Gly		
				405					410						415		
Leu	Glu	Pro	Asn	Ile	Leu	Thr	Lys	Gln	Lys	Leu	Glu	Asn	Leu	Leu	Leu		
			420					425					430				
Ser	Ile	Lys	Gln	Ser	Lys	Asn	Leu	Lys	Phe	Leu	Arg	Leu	Asn	Phe	Tyr		
		435					440					445					
Thr	Tyr	Val	Ala	Gln	Glu	Thr	Ser	Arg	Lys	Gln	Ile	Leu	Lys	Gln	Ala		
	450					455					460						
Thr	Thr	Ile	Lys	Asn	Leu	Lys	Asn	Asn	Lys	Asn	Gln	Glu	Glu	Thr	Pro		
465					470				475						480		
Glu	Thr	Lys	Asp	Glu	Thr	Pro	Ser	Glu	Ser	Thr	Ser	Gly	Met	Lys	Phe		
			485						490					495			
Phe	Asp	His	Leu	Ser	Glu	Leu	Thr	Glu	Leu	Glu	Asp	Phe	Ser	Val	Asn		
			500					505					510				
Leu	Gln	Ala	Thr	Gln	Glu	Ile	Tyr	Asp	Ser	Leu	His	Lys	Leu	Leu	Ile		
		515					520					525					
Arg	Ser	Thr	Asn	Leu	Lys	Lys	Phe	Lys	Leu	Ser	Tyr	Lys	Tyr	Glu	Met		
	530					535					540						
Glu	Lys	Ser	Lys	Met	Asp	Thr	Phe	Ile	Asp	Leu	Lys	Asn	Ile	Tyr	Glu		
545				550					555						560		
Thr	Leu	Asn	Asn	Leu	Lys	Arg	Cys	Ser	Val	Asn	Ile	Ser	Asn	Pro	His		
				565					570					575			
Gly	Asn	Ile	Ser	Tyr	Glu	Leu	Thr	Asn	Lys	Asp	Ser	Thr	Phe	Tyr	Lys		
		580						585					590				
Phe	Lys	Leu	Thr	Leu	Asn	Gln	Glu	Leu	Gln	His	Ala	Lys	Tyr	Thr	Phe		
		595					600					605					
Lys	Gln	Asn	Glu	Phe	Gln	Phe	Asn	Asn	Val	Lys	Ser	Ala	Lys	Ile	Glu		
	610					615					620						
Ser	Ser	Ser	Leu	Glu	Ser	Leu	Glu	Asp	Ile	Asp	Ser	Leu	Cys	Lys	Ser		
625					630				635					640			
Ile	Ala	Ser	Cys	Lys	Asn	Leu	Gln	Asn	Val	Asn	Ile	Ile	Ala	Ser	Leu		
			645						650					655			
Leu	Tyr	Pro	Asn	Asn	Ile	Gln	Lys	Asn	Pro	Phe	Asn	Lys	Pro	Asn	Leu		
			660					665					670				
Leu	Phe	Phe	Lys	Gln	Phe	Glu	Gln	Leu	Lys	Asn	Leu	Glu	Asn	Val	Ser		
		675					680					685					
Ile	Asn	Cys	Ile	Leu	Asp	Gln	His	Ile	Leu	Asn	Ser	Ile	Ser	Glu	Phe		
	690					695					700						
Leu	Glu	Lys	Asn	Lys	Lys	Ile	Lys	Ala	Phe	Ile	Leu	Lys	Arg	Tyr	Tyr		
705					710					715					720		

Leu Leu Gln Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln
 725 730 735
 Gln Leu Pro Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu
 740 745 750
 Leu Thr Val Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln
 755 760 765
 Lys Ala Phe Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln
 770 775 780
 Thr Leu Gln Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser
 785 790 795 800
 Ile Lys Lys Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr
 805 810 815
 Leu Arg Leu Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn
 820 825 830
 Glu Glu Ile Gln Glu Leu Leu Lys
 835 840

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
 1 5 10 15
 Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
 20 25 30
 Leu Leu

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser
1 5 10 15
Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu
20 25 30
Gly Phe Leu
35

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln Glu Asn
1 5 10 15
Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg Glu Asn
20 25 30
Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr
35 40

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Gln Asp Tyr Cys Asp Trp Ile Gly Ile Ser Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Lys Asn Arg Asn Leu His Cys Thr Tyr Ile Asp Tyr Lys Lys Ala Phe
1 5 10 15
Asp Ser Ile Pro His Ser Trp Leu Ile Gln Val Leu Glu Ile Tyr Lys
20 25 30
Ile Asn

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Arg Gln Ile Ala Ile Lys Lys Gly Ile Tyr Gln Gly Asp Ser Leu Ser
1 5 10 15
Pro Leu Trp Phe Cys Leu Ala Leu Asn Pro Leu Ser His Gln Leu His
20 25 30
Asn Asp Arg
35

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

His Leu Ile Tyr Met Asp Asp Ile Lys Leu Tyr Ala Lys Asn Asp Lys
1 5 10 15
Glu Met Lys Lys Leu Ile Asp Thr Thr Thr Ile Phe Ser Asn Asp Ile
20 25 30
Ser Met Gln Phe Gly Leu Asp Lys Cys Lys Thr
35 40

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Lys Cys Leu Tyr Lys Tyr Leu Gly Phe Gln Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

Phe Gly Gly Ser Asn Trp Phe Arg Glu Val Asp Leu Lys Lys Cys Phe
1 5 10 15

Asp Thr Ile Ser His Asp Leu Ile Ile Lys Glu Leu Lys Arg Tyr Ile
 20 25 30

Ser Asp

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

His Val Pro Val Gly Pro Arg Val Cys Val Gln Gly Ala Pro Thr Ser
1 5 10 15

Pro Ala Leu Cys Asn Ala Val Leu Leu Arg Leu Asp Arg Arg Leu Ala
 20 25 30

Gly Leu Ala
 35

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

Tyr	Val	Arg	Tyr	Ala	Asp	Asp	Ile	Leu	Ile	Gly	Val	Leu	Gly	Ser	Lys
1				5					10					15	

Asn

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Lys	Ile	Ile	Lys	Arg	Asp	Leu	Asn	Asn	Phe	Leu	Asn	Ser	Leu	Gly	Leu
1				5					10					15	

Thr	Ile	Asn	Glu	Glu	Lys	Thr	Leu	Ile
			20					25

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

Glu	Thr	Pro	Ala	Arg	Phe	Leu	Gly	Tyr	Asn	Ile
1				5					10	

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr
1 5 10 15

Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr
 20 25 30

Ile Pro

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser
1 5 10 15

Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg
 20 25 30

Lys Gln Asn
 35

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser His Leu Glu Ile
1 5 10 15
Gly

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly
1 5 10 15
Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp
20 25 30
Met Gly Tyr Glu Leu
35

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Val Leu Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr
1 5 10 15
Asp Ser Ile Pro Arg Met Glu Cys Met Arg Ile Leu Lys Asp Ala Leu
20 25 30
Lys Asn

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Lys Cys Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser
1 5 10 15
Ala Pro Ile Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser
20 25 30
Glu Phe Lys
35

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln Gln
1 5 10 15
Gln Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr
20 25 30
Asn Ala Lys Ala Asn Arg
35

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

Ile Arg Ser Lys Ser Ser Lys Gly Ile Phe Arg
1 5 10

(2) INFORMATION FOR SEO ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 6
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- ```
(A) NAME/KEY: Modified-site
(B) LOCATION: 10
(D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"
```

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 13  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1 5 10

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Gln | Gly | Xaa | Xaa | Xaa | Ser | Pro |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8..10
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Xaa Xaa Xaa Tyr Xaa Asp Asp Xaa Xaa Xaa  
1 5 10

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Gly Xaa Xaa Xaa Xaa Xaa Xaa Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 3  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid,  
 selected from Ala, Leu, Ile, Val, Pro,  
 Phe, Trp or Met"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 6  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid,  
 selected from Ala, Leu, Ile, Val, Pro,  
 Phe, Trp or Met"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 8  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid,  
 selected from Ala, Leu, Ile, Val, Pro,  
 Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Xaa Xaa Xaa Leu Gly Xaa Xaa Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Tyr Tyr Tyr Arg Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 9 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Gly Lys Leu Arg Ile Ile Pro Lys Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

Phe Arg Pro Ile Met Thr Phe  
1 5

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe  
1 5 10 15  
Tyr Arg Lys Ser Val Trp Ser Lys  
20

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Arg Gln His Leu Lys Arg Val Gln Leu Arg Asp Val Ser Glu Ala Glu  
1 5 10 15  
Val Arg Gln His Arg Glu Ala  
20

(2) INFORMATION FOR SEQ ID NO:258:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 27 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Arg | Thr | Phe | Arg | Arg | Glu | Lys | Arg | Ala | Glu | Arg | Leu | Thr | Ser | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Lys | Ala | Leu | Phe | Ser | Val | Leu | Asn | Tyr | Glu |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:259:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 28 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Lys | Phe | Leu | His | Trp | Leu | Met | Ser | Val | Tyr | Val | Val | Glu | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Ser | Phe | Phe | Tyr | Val | Thr | Glu | Thr | Thr | Phe | Gln |     |     |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:260:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 30 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Phe | Phe | Tyr | Arg | Lys | Ser | Val | Trp | Ser | Lys | Leu | Gln | Ser | Ile | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Arg | Gln | His | Leu | Lys | Arg | Val | Gln | Leu | Arg | Asp | Val | Ser |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

(2) INFORMATION FOR SEQ ID NO:261:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ala | Leu | Leu | Thr | Ser | Arg | Leu | Arg | Phe | Ile | Pro | Lys | Pro | Asp | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Leu | Arg | Pro | Ile | Val | Asn | Met | Asp | Tyr | Val | Val |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

YARACHAARG GHATYCCHYA RGG

23

(2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

NGTNATDARD ARRTARTCRT C

21

(2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Gln Thr Lys Gly Ile Pro Gln Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

Asp Asp Tyr Leu Leu Ile Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe  
1 5 10 15  
Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu  
20 25 30  
Ser Met Asn Pro Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr  
35 40 45  
Asp Asp Tyr Leu Leu Ile Thr  
50 55

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

```
Ser Ile Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile
1 5 10 15
Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys Gly Ser Val Leu Leu Arg
 20 25 30
Val Val
```

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 49 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

```
Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile Val Asp Leu
1 5 10 15
Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys Ala Ser Pro
 20 25 30
Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile
 35 40 45
Ser
```

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

```
Gln Lys Val Gly Ile Pro Gln Gly
1 5
```

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

23

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 146 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| AGACCAAAGG | AATTCATCA  | GGCTCAATTC | TGTCATCTTT | TTTGTGTCAT | TTCTATATGG | 60  |
| AAGATTTGAT | TGATGAATAC | CTATCGTTTA | CGAAAAAGAA | AGGATCAGTG | TTGTTACGAG | 120 |
| TAGTCGACGA | CTACCTCCTC | ATCACC     |            |            |            | 146 |

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 47 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gly | Ile | Pro | Ser | Gly | Ser | Ile | Leu | Ser | Ser | Phe | Leu | Cys | His | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Met | Glu | Asp | Leu | Ile | Asp | Glu | Tyr | Leu | Ser | Phe | Thr | Lys | Lys | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ser | Val | Leu | Leu | Arg | Val | Val | Asp | Asp | Tyr | Leu | Leu | Ile | Thr |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

GACGATTTC TCTTTATAAC A

21

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Asp Asp Phe Leu Phe Ile Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr  
1 5 10 15  
Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys  
20 25 30  
Asp Ile Trp  
35

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

Ala Val Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg Leu Ile Thr  
1 5 10 15

Asn Leu Arg Lys Arg Phe  
20

(2) INFORMATION FOR SEQ ID NO:277:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile  
1 5 10 15  
Lys Gln Asp Leu Met Phe Arg Ile Val Lys  
20 25

(2) INFORMATION FOR SEQ ID NO:278:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser Ser Phe  
1 5 10 15  
Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu Ser Phe  
20 25 30

(2) INFORMATION FOR SEQ ID NO:279:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys  
1 5 10 15

Lys Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys  
                   20                  25                  30

His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn Phe Glu Asn  
           35                  40                  45

Ser

(2) INFORMATION FOR SEQ ID NO:280:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Trp Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr  
   1                  5                  10                  15

Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp  
           20                  25                  30

Thr Trp

(2) INFORMATION FOR SEQ ID NO:281:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu Phe Arg Ile  
   1                  5                  10                  15

Ile Ala Ile Pro Cys Arg Gly Ala Asp  
           20                  25

(2) INFORMATION FOR SEQ ID NO:282:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Leu | Tyr | Phe | Met | Lys | Phe | Asp | Val | Lys | Ser | Cys | Tyr | Asp | Ser | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Arg | Met | Glu | Cys | Met | Arg | Ile | Leu | Lys |     |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ile | Arg | Glu | Asp | Gly | Leu | Phe | Gln | Gly | Ser | Ser | Leu | Ser | Ala | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Val | Asp | Leu | Val | Tyr | Asp | Asp | Leu | Leu | Glu | Phe | Tyr | Ser | Glu | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Leu | Lys | Leu | Ala | Asp | Asp | Phe | Leu | Ile | Ile | Ser | Thr | Asp | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Gln | Val | Ile | Asn | Ile | Lys | Lys | Leu | Ala | Met | Gly | Gly | Phe | Gln | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Asn | Ala | Lys | Ala | Asn | Arg | Asp | Lys | Ile | Leu | Ala | Val | Ser | Ser | Gln |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr  
1 5 10 15  
Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys  
20 25 30  
Asn Ile Trp  
35

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met  
1 5 10 15  
Thr Phe Asn Lys Lys Ile Val  
20

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser Val  
1 5 10 15  
Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys  
20 25

(2) INFORMATION FOR SEQ ID NO:288:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 32 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Lys | Gln | Thr | Lys | Gly | Ile | Pro | Gln | Gly | Leu | Cys | Val | Ser | Ser | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ser | Ser | Phe | Tyr | Tyr | Ala | Thr | Leu | Glu | Glu | Ser | Ser | Leu | Gly | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

(2) INFORMATION FOR SEQ ID NO:289:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 49 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Met | Arg | Leu | Thr | Asp | Asp | Tyr | Leu | Leu | Ile | Thr | Thr | Gln | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Asn | Ala | Val | Leu | Phe | Ile | Glu | Lys | Leu | Ile | Asn | Val | Ser | Arg | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Gly | Phe | Lys | Phe | Asn | Met | Lys | Lys | Leu | Gln | Thr | Ser | Phe | Pro | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:290:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 4 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 1  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid,  
 selected from Ala, Leu, Ile, Val, Pro,  
 Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Xaa Pro Gln Gly  
1

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 3  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid,  
 selected from Ala, Leu, Ile, Val, Pro,  
 Phe, Trp or Met"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 4  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid,  
 selected from Ala, Leu, Ile, Val, Pro,  
 Phe, Trp or Met"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 5  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid,  
 selected from Ala, Leu, Ile, Val, Pro,  
 Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Asp Asp Xaa Xaa Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:292:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln  
1                    5                    10                    15  
  
Lys Ser Tyr Ser Lys Thr  
                    20

(2) INFORMATION FOR SEQ ID NO:293:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 30 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro Lys Lys  
1                    5                    10                    15  
  
Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val  
                    20                    25                    30

(2) INFORMATION FOR SEQ ID NO:294:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 27 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser  
1                    5                    10                    15  
  
Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys  
                    20                    25

(2) INFORMATION FOR SEQ ID NO:295:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 27 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Gly | Lys | Phe | Tyr | Lys | Gln | Thr | Lys | Gly | Ile | Pro | Gln | Gly | Leu | Cys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ser | Ser | Ile | Leu | Ser | Ser | Phe | Tyr | Tyr | Ala |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:296:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Asn | Val | Asn | Leu | Leu | Met | Arg | Leu | Thr | Asp | Asp | Tyr | Leu | Leu | Ile |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Thr | Thr | Gln | Glu | Asn | Asn |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:297:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Val | Ser | Arg | Glu | Asn | Gly | Phe | Lys | Phe | Asn | Met | Lys | Lys | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |

(2) INFORMATION FOR SEQ ID NO:298:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr Ile Thr Glu Ser Ser  
1                    5                    10                    15  
  
Asp Leu Arg Asn Arg Thr  
                    20

(2) INFORMATION FOR SEQ ID NO:299:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 30 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

Gln Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys  
1                    5                    10                    15  
  
Asn Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu  
                    20                    25                    30

(2) INFORMATION FOR SEQ ID NO:300:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 27 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg  
1                    5                    10                    15  
  
Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys  
                    20                    25

(2) INFORMATION FOR SEQ ID NO:301:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 27 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Asn | Ser | Gln | Tyr | Leu | Gln | Lys | Val | Gly | Ile | Pro | Gln | Gly | Ser | Ile |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Ser | Ser | Phe | Leu | Cys | His | Phe | Tyr | Met | Glu |     |     |     |     |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:302:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Lys | Gly | Ser | Val | Leu | Leu | Arg | Val | Val | Asp | Asp | Phe | Leu | Phe | Ile |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Thr | Val | Asn | Lys | Lys | Asp |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:303:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Leu | Ser | Leu | Arg | Gly | Phe | Glu | Lys | His | Asn | Phe | Ser | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |

(2) INFORMATION FOR SEQ ID NO:304:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr Glu Ile Ser  
1                    5                    10                    15  
  
Ser Thr Val Thr Ile Val  
                    20

(2) INFORMATION FOR SEQ ID NO:305:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 32 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

Thr Leu Ser Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys  
1                    5                    10                    15  
  
Ser Asn Asn Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp  
                    20                    25                    30

(2) INFORMATION FOR SEQ ID NO:306:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 27 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser  
1                    5                    10                    15  
  
Ile Pro Arg Met Glu Cys Met Arg Ile Leu Lys  
                    20                    25

(2) INFORMATION FOR SEQ ID NO:307:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 27 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asp | Lys | Cys | Tyr | Ile | Arg | Glu | Asp | Gly | Leu | Phe | Gln | Gly | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ser | Ala | Pro | Ile | Val | Asp | Leu | Val | Tyr | Asp |     |     |     |     |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:308:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gln | Asp | Thr | Leu | Ile | Leu | Lys | Leu | Ala | Asp | Asp | Phe | Leu | Ile | Ile |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Thr | Asp | Gln | Gln | Gln |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:309:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Lys | Leu | Ala | Met | Gly | Gly | Phe | Gln | Lys | Tyr | Asn | Ala | Lys | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |

(2) INFORMATION FOR SEQ ID NO:310:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr  
1                    5                    10                    15  
  
Phe Gln Lys Asn Arg Leu  
                    20

(2) INFORMATION FOR SEQ ID NO:311:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 30 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro  
1                    5                    10                    15  
  
Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly  
                    20                    25                    30

(2) INFORMATION FOR SEQ ID NO:312:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 27 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr  
1                    5                    10                    15  
  
Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala  
                    20                    25

(2) INFORMATION FOR SEQ ID NO:313:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ala | Thr | Ser | Tyr | Val | Gln | Cys | Gln | Gly | Ile | Pro | Gln | Gly | Ser | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ser | Thr | Leu | Leu | Cys | Ser | Leu | Cys | Tyr | Gly |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:314:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Arg | Asp | Gly | Leu | Leu | Leu | Arg | Leu | Val | Asp | Asp | Phe | Leu | Leu | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Pro | His | Leu | Thr | His |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:315:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Arg | Thr | Leu | Val | Arg | Gly | Val | Pro | Glu | Tyr | Gly | Cys | Val | Val |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ala | Ala | Leu | Arg | Pro | Ala | Ala | His | Val | Gly | Ser | Pro | Gly | Pro | Gly | His |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Pro | Arg | Asp | Ala | Ala | Arg | Ser | Pro | Leu | Pro | Ser | Arg | Ala | Leu | Pro | Ala |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala | Gln | Pro | Leu | Pro | Arg | Gly | Ala | Ala | Ala | Gly | His | Val | Arg | Ala | Ala |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Pro | Gly | Ala | Pro | Gly | Leu | Ala | Ala | Gly | Ala | Ala | Arg | Gly | Pro | Gly | Gly |  |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |
| Phe | Pro | Arg | Xaa | Gly | Gly | Pro | Xaa | Xaa | Gly | Val | Arg | Ala | Leu | Gly | Xaa |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Xaa | Ala | Ala | Pro | Arg | Arg | Pro | Leu | Leu | Pro | Pro | Gly | Val | Leu | Pro | Glu |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Xaa | Xaa | Gly | Gly | Pro | Ser | Ala | Ala | Xaa | Ala | Val | Arg | Xaa | Arg | Arg | Glu |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| Xaa | Arg | Ala | Gly | Leu | Arg | Leu | Arg | Ala | Ala | Gly | Arg | Gly | Pro | Arg | Gly |  |
|     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |     |  |
| Pro | Pro | Arg | Gly | Leu | His | His | Gln | Arg | Ala | Gln | Leu | Pro | Ala | Gln | His |  |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |  |
| Gly | Asp | Arg | Arg | Thr | Ala | Gly | Glu | Arg | Gly | Val | Gly | Ala | Ala | Ala | Ala |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Pro | Arg | Gly | Arg | Arg | Ala | Gly | Ser | Pro | Ala | Gly | Thr | Leu | Arg | Xaa |     |  |
|     |     |     | 165 |     |     |     | 170 |     |     |     |     | 175 |     |     |     |  |
| Xaa | Cys | Ala | Gly | Gly | Ser | Gln | Leu | Arg | Leu | Pro | Xaa | Val | Arg | Ala | Ala |  |
|     | 180 |     |     |     | 185 |     |     |     |     |     |     | 190 |     |     |     |  |
| Ala | Val | Pro | Ala | Arg | Arg | Cys | Xaa | Ser | Gly | Pro | Ala | Pro | Ala | Thr | Arg |  |
|     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |     |  |
| Xaa | Trp | Thr | Arg | Xaa | Arg | Leu | Gly | Ser | Asn | Gly | Pro | Gly | Thr | Ile | Ala |  |
|     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |  |
| Ser | Gly | Arg | Pro | Gly | Ser | Pro | Trp | Ala | Ala | Ser | Pro | Gly | Cys | Glu | Glu |  |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |  |
| Ala | Arg | Gly | Gln | Cys | Gln | Pro | Lys | Ser | Ala | Val | Ala | Gln | Glu | Ala | Gln |  |
|     |     |     | 245 |     |     |     | 250 |     |     |     |     | 255 |     |     |     |  |

Ala Trp Arg Cys Pro  
260

(2) INFORMATION FOR SEQ ID NO:317:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Ala Gly Ala Asp Ala Arg Trp Ala Gly Val Leu Gly Pro Pro Gly Gln  
1                   5                   10                   15  
Asp Ala Trp Thr Glu  
20

(2) INFORMATION FOR SEQ ID NO:318:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 82 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Pro Trp Phe Leu Cys Gly Val Thr Cys Gln Thr Arg Arg Arg Ser His  
1                   5                   10                   15  
Leu Phe Gly Gly Cys Ala Leu Trp His Ala Pro Leu Pro Pro Ile Arg  
20                   25                   30  
Gly Pro Pro Ala Pro Arg Gly Pro Pro Ile His Ile Ala Ala Thr Thr  
35                   40                   45  
Ser Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe  
50                   55                   60  
Leu Tyr Ser Ser Gly Asp Lys Xaa Thr Ala Xaa Leu Leu Pro Thr Gln  
65                   70                   75                   80  
Tyr Ile

(2) INFORMATION FOR SEQ ID NO:319:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 153 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

```
Leu Ala Phe Gly Arg Phe Val Glu Thr Xaa Phe Leu Val Pro Gly Leu
1 5 10 15
Gly Cys Gln Asp Ser Pro Gln Val Ala Pro Pro Ala Pro Ala Xaa Leu
20 25 30
Ala Asn Ala Ala Pro Val Ser Gly Ala Ala Trp Glu Pro Arg Ala Val
35 40 45
Pro Leu Arg Gly Val Pro Gln Asp Ala Leu Pro Ala Ala Ser Cys Gly
50 55 60
His Pro Ser Ser Arg Cys Leu Cys Pro Gly Glu Ala Pro Gly Leu Cys
65 70 75 80
Gly Gly Pro Arg Gly Gly Gly Thr Gln Thr Pro Val Ala Trp Cys Ser
85 90 95
Cys Ser Ala Ser Thr Ala Ala Pro Gly Arg Cys Thr Ala Ser Cys Gly
100 105 110
Pro Ala Cys Ala Gly Trp Cys Pro Gln Ala Ser Gly Ala Pro Gly Thr
115 120 125
Thr Asn Ala Ala Ser Ser Gly Thr Pro Arg Ser Ser Ser Pro Trp Gly
130 135 140
Ser Met Pro Ser Ser Arg Cys Arg Ser
145 150
```

(2) INFORMATION FOR SEQ ID NO:320:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 35 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

```
Ala Cys Gly Thr Ala Leu Gly Cys Ala Gly Ala Gln Gly Leu Ala Val
1 5 10 15
```

Phe Arg Pro Gln Ser Thr Val Cys Val Arg Arg Ser Trp Pro Ser Ser  
                   20                  25                  30  
 Cys Thr Gly  
                   35

(2) INFORMATION FOR SEQ ID NO:321:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

Val Cys Thr Ser Ser Ser Cys Ser Gly Leu Ser Phe Met Ser Arg Arg  
 1                  5                  10                  15  
 Pro Arg Phe Lys Arg Thr Gly Ser Phe Ser Thr Gly Arg Val Ser Gly  
                   20                  25                  30  
 Ala Ser Cys Lys Ala Leu Glu Ser Asp Ser Thr  
                   35                  40

(2) INFORMATION FOR SEQ ID NO:322:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Arg Gly Cys Ser Cys Gly Ser Cys Arg Lys Gln Arg Ser Gly Ser Ile  
 1                  5                  10                  15  
 Gly Lys Pro Gly Pro Pro Cys  
                   20

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Arg Pro Asp Ser Ala Ser Ser Pro Ser Leu Thr Gly Cys Gly Arg Leu  
1                      5                      10                      15

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 23 amino acids  
  (B) TYPE: amino acid  
  (C) STRANDEDNESS:  
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Thr Trp Thr Thr Ser Trp Glu Pro Glu Arg Ser Ala Glu Lys Arg Gly  
1                      5                      10                      15  
  
Pro Ser Val Ser Pro Arg Gly  
                    20

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 54 amino acids  
  (B) TYPE: amino acid  
  (C) STRANDEDNESS:  
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

Arg His Cys Ser Ala Cys Ser Thr Thr Ser Gly Arg Gly Ala Pro Ala  
1                      5                      10                      15  
  
Ser Trp Ala Pro Leu Cys Trp Ala Trp Thr Ile Ser Thr Gly Pro Gly  
                    20                      25                      30  
  
Ala Pro Ser Cys Cys Val Cys Gly Pro Arg Thr Arg Arg Leu Ser Cys  
                    35                      40                      45  
  
Thr Leu Ser Arg Trp Met  
                    50

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 52 amino acids  
  (B) TYPE: amino acid  
  (C) STRANDEDNESS:  
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

Gln Thr Ser Ser Arg Thr Cys Asp Ser Ser Trp Leu Thr Cys Arg Xaa  
1 5 10 15  
Thr Ala Arg

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Gly Met Pro Ser Ser Ser Ser Arg Ala Pro Pro  
1 5 10

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 74 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

```
Met Arg Pro Ala Val Ala Ser Ser Thr Ser Ser Tyr Ala Ser Cys Ala
1 5 10 15

Thr Thr Pro Cys Ala Ser Gly Ala Ser Pro Thr Ser Ser Ala Arg Gly
 20 25 30

Ser Arg Arg Ala Pro Ser Ser Pro Arg Cys Ser Ala Ala Cys Ala Thr
 35 40 45

Ala Thr Trp Arg Thr Ser Cys Leu Arg Gly Phe Gly Gly Thr Gly Cys
50 55 60

Ser Cys Val Trp Trp Met Ile Ser Cys Trp
65 70
```

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

```
His Leu Thr Ser Pro Thr Arg Lys Pro Ser Ser Gly Pro Trp Ser Glu
1 5 10 15

Val Ser Leu Ser Met Ala Ala Trp
 20
```

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

```
Thr Cys Gly Arg Gln Trp
1 5
```

(2) INFORMATION FOR SEQ ID NO:332:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 70 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

```
Lys Thr Arg Pro Trp Val Ala Arg Leu Leu Phe Arg Cys Arg Pro Thr
1 5 10 15

Ala Tyr Ser Pro Gly Ala Ala Cys Cys Trp Ile Pro Gly Pro Trp Arg
 20 25 30

Cys Arg Ala Thr Thr Pro Ala Met Pro Gly Pro Pro Ser Glu Pro Val
 35 40 45

Ser Pro Ser Thr Ala Ala Ser Arg Leu Gly Gly Thr Cys Val Ala Asn
50 55 60

Ser Leu Gly Ser Cys Gly
65 70
```

(2) INFORMATION FOR SEQ ID NO:333:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 10 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

```
Ser Val Thr Ala Cys Phe Trp Ile Cys Arg
1 5 10
```

(2) INFORMATION FOR SEQ ID NO:334:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 55 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

```
Thr Ala Ser Arg Arg Cys Ala Pro Thr Ser Thr Arg Ser Ser Cys Cys
1 5 10 15
```

Arg Arg Thr Gly Phe Thr His Val Cys Cys Ser Ser His Phe Ile Ser  
20 25 30

Lys Phe Gly Arg Thr Pro His Phe Ser Cys Ala Ser Ser Leu Thr Arg  
35 40 45

Pro Pro Ser Ala Thr Pro Ser  
50 55

(2) INFORMATION FOR SEQ ID NO:335:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

Lys Pro Arg Thr Gln Gly Cys Arg Trp Gly Pro Arg Ala Pro Pro Ala  
1 5 10 15

Leu Cys Pro Pro Arg Pro Cys Ser Gly Cys Ala Thr Lys His Ser Cys  
20 25 30

Ser Ser

(2) INFORMATION FOR SEQ ID NO:336:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

Leu Asp Thr Val Ser Pro Thr Cys His Ser Trp Gly His Ser Gly Gln  
1 5 10 15

Pro Arg Arg Ser  
20

(2) INFORMATION FOR SEQ ID NO:337:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

Val Gly Ser Ser Arg Gly Arg Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 61 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

Leu Pro Trp Arg Pro Gln Pro Thr Arg His Cys Pro Gln Thr Ser Arg  
1 5 10 15  
Pro Ser Trp Thr Asp Gly His Pro Pro Thr Ala Arg Pro Arg Ala Asp  
20 25 30  
Thr Ser Ser Pro Val Thr Pro Gly Ser Thr Ser Gln Gly Gly Arg Gly  
35 40 45  
Gly Pro His Pro Gly Pro His Arg Trp Glu Ser Glu Ala  
50 55 60

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

Val Ser Val Trp Pro Arg Pro Ala Cys Pro Ala Glu Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Gly Leu Ser Glu Cys Pro Ala Lys Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Val Ser Ser Thr Pro Ala Val Phe Thr Ser Pro Gln Ala Gly Ala Arg  
1 5 10 15  
Leu His Pro Arg Ala Ser Phe Ser Ser Pro Gly Ala Arg Leu Pro Leu  
20 25 30  
Pro Thr

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Ser Ile Pro Arg Phe Ala Ile Val His Pro Ser Pro Cys Pro Pro Leu  
1 5 10 15  
Pro Ser Thr Pro Thr Ile Gln Val Glu Thr Leu Arg Arg Thr Leu Gly  
20 25 30  
Ala Leu Gly Ile Trp Ser Asp Gln Arg Cys Ala Leu Tyr Thr Gly Glu  
35 40 45  
Asp Pro Ala Pro Gly Trp Gly Ser Leu Trp Val Lys Leu Gly Gly Gly  
50 55 60  
Ala Val Gly Val Lys Tyr  
65 70

(2) INFORMATION FOR SEQ ID NO:343:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Tyr | Glu | Phe | Phe | Ser | Phe | Glu | Lys | Lys | Lys | Lys | Lys | Lys | Lys | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

(2) INFORMATION FOR SEQ ID NO:344:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 222 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Arg | Cys | Val | Leu | Leu | Arg | Thr | Trp | Glu | Ala | Leu | Ala | Pro | Ala | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Ala | Met | Pro | Arg | Ala | Pro | Arg | Cys | Arg | Ala | Val | Arg | Ser | Leu | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ser | His | Tyr | Arg | Glu | Val | Leu | Pro | Leu | Ala | Thr | Phe | Val | Arg | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Gly | Pro | Gln | Gly | Trp | Arg | Leu | Val | Gln | Arg | Gly | Asp | Pro | Ala | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Arg | Ala | Xaa | Val | Ala | Xaa | Cys | Xaa | Val | Cys | Val | Pro | Trp | Xaa | Xaa |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Xaa | Xaa | Pro | Pro | Ala | Ala | Pro | Ser | Phe | Arg | Gln | Val | Ser | Cys | Leu | Xaa |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Xaa | Leu | Val | Ala | Arg | Val | Leu | Xaa | Xaa | Leu | Cys | Xaa | Arg | Gly | Ala | Xaa |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Val | Leu | Ala | Phe | Gly | Phe | Ala | Leu | Leu | Asp | Gly | Ala | Arg | Gly | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Pro | Glu | Ala | Phe | Thr | Thr | Ser | Val | Arg | Ser | Tyr | Leu | Pro | Asn | Thr |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Thr | Asp | Ala | Leu | Arg | Gly | Ser | Gly | Ala | Trp | Gly | Leu | Leu | Leu | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Val | Gly | Asp | Asp | Val | Leu | Val | His | Leu | Leu | Ala | Arg | Cys | Ala | Xaa |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Val | Leu | Val | Xaa | Pro | Ser | Cys | Ala | Tyr | Xaa | Val | Cys | Gly | Pro | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Tyr | Gln | Leu | Gly | Ala | Ala | Thr | Gln | Ala | Arg | Pro | Pro | Pro | His | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Xaa | Gly | Pro | Glu | Xaa | Val | Trp | Asp | Pro | Thr | Gly | Leu | Glu | Pro |     |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:345:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 330 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Gln | Gly | Gly | Arg | Gly | Pro | Pro | Gly | Leu | Pro | Ala | Pro | Gly | Ala | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Arg | Gly | Gly | Ser | Ala | Ser | Arg | Ser | Leu | Pro | Leu | Pro | Lys | Arg | Pro |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Arg | Arg | Gly | Ala | Ala | Pro | Glu | Pro | Glu | Arg | Thr | Pro | Val | Gly | Gln | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ser | Trp | Ala | His | Pro | Gly | Arg | Thr | Pro | Gly | Pro | Ser | Asp | Arg | Gly | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Val | Val | Ser | Pro | Ala | Arg | Pro | Ala | Glu | Glu | Ala | Thr | Ser | Leu | Glu |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Ala | Leu | Ser | Gly | Thr | Arg | His | Ser | His | Pro | Ser | Val | Gly | Arg | Gln |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| His | His | Ala | Gly | Pro | Pro | Ser | Thr | Ser | Arg | Pro | Pro | Arg | Pro | Gly | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Leu | Val | Pro | Arg | Cys | Thr | Pro | Arg | Pro | Ser | Thr | Ser | Ser | Thr | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Ala | Thr | Xaa | Thr | Leu | Arg | Pro | Ser | Phe | Leu | Leu | Asn | Ile | Ser | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Gln | Pro | Asp | Trp | Arg | Ser | Gly | Gly | Ser | Trp | Arg | Xaa | Ser | Phe | Trp |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Phe | Gln | Ala | Leu | Asp | Ala | Arg | Ile | Pro | Arg | Arg | Leu | Pro | Arg | Leu | Pro |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Gln | Arg | Tyr | Trp | Gln | Met | Arg | Pro | Leu | Phe | Leu | Glu | Leu | Leu | Gly | Asn |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |

His Ala Gln Cys Pro Tyr Gly Val Phe Leu Lys Thr His Cys Pro Leu  
 195 200 205  
 Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro  
 210 215 220  
 Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Glu His Arg Pro Pro Ser  
 225 230 235 240  
 Pro Gly Ala Ala Ala Pro Pro Ala Gln Gln Pro Leu Ala Gly Val Arg  
 245 250 255  
 Leu Arg Ala Gly Leu Pro Ala Pro Ala Gly Ala Pro Arg Pro Leu Gly  
 260 265 270  
 Leu Gln Ala Gln Arg Thr Pro Leu Pro Gln Glu His Gln Glu Val His  
 275 280 285  
 Leu Pro Gly Glu Ala Cys Gln Ala Leu Ala Ala Gly Ala Asp Val Glu  
 290 295 300  
 Asp Glu Arg Ala Gly Leu Arg Leu Ala Ala Gln Glu Pro Arg Gly Trp  
 305 310 315 320  
 Leu Cys Ser Gly Arg Arg Ala Pro Ser Ala  
 325 330

(2) INFORMATION FOR SEQ ID NO:346:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 89 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Gly Asp Pro Gly Gln Val Pro Ala Leu Ala Asp Glu Cys Val Arg Arg  
 1 5 10 15  
 Arg Ala Ala Gln Val Phe Leu Leu Cys His Gly Asp His Val Ser Lys  
 20 25 30  
 Glu Gln Ala Leu Phe Leu Pro Glu Glu Cys Leu Glu Gln Val Ala Lys  
 35 40 45  
 His Trp Asn Gln Thr Ala Leu Glu Glu Gly Ala Ala Ala Gly Ala Val  
 50 55 60  
 Gly Ser Arg Gly Gln Ala Ala Ser Gly Ser Gln Ala Arg Pro Ala Asp  
 65 70 75 80  
 Val Gln Thr Pro Leu His Pro Gln Ala  
 85

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Arg Ala Ala Ala Asp Cys Glu His Gly Leu Arg Arg Gly Ser Gln Asn  
1                      5                      10                      15  
Val Pro Gln Arg Lys Glu Gly Arg Ala Ser His Leu Glu Gly Glu Gly  
                    20                      25                      30  
Thr Val Gln Arg Ala Gln Leu Arg Ala Gly Ala Ala Pro Arg Pro Pro  
                    35                      40                      45  
Gly Arg Leu Cys Ala Gly Pro Gly Arg Tyr Pro Gln Gly Leu Ala His  
50                      55                      60  
Leu Arg Ala Ala Cys Ala Gly Pro Gly Pro Ala Ala  
65                      70                      75

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

Ala Val Leu Cys Gln Gly Gly Cys Asp Gly Arg Val Arg His His Pro  
1                      5                      10                      15  
Pro Gly Gln Ala His Gly Gly His Arg Gln His His Gln Thr Pro Glu  
                    20                      25                      30  
His Val Leu Arg Ala Ser Val Cys Arg Gly Pro Glu Gly Arg Pro Trp  
                    35                      40                      45  
Ala Arg Pro Gln Gly Leu Gln Glu Pro Arg Leu Tyr Leu Asp Arg Pro  
50                      55                      60  
Pro Ala Val His Ala Thr Val Arg Gly Ser Pro Ala Gly Xaa Gln Pro  
65                      70                      75                      80  
Ala Glu Gly Cys Arg Arg His Arg Ala Glu Leu Leu Pro Glu  
                    85                      90

(2) INFORMATION FOR SEQ ID NO:349:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 68 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

```
Gly Gln Gln Trp Pro Leu Arg Arg Leu Pro Thr Leu His Val Pro Pro
1 5 10 15

Arg Arg Ala His Gln Gly Gln Val Leu Arg Pro Val Pro Gly Asp Pro
 20 25 30

Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg
 35 40 45

His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro
 50 55 60

Ala Phe Gly Gly
65
```

(2) INFORMATION FOR SEQ ID NO:350:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 23 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

```
Phe Leu Val Gly Asp Thr Ser Pro His Pro Arg Glu Asn Leu Pro Gln
1 5 10 15

Asp Pro Gly Pro Arg Cys Pro
 20
```

(2) INFORMATION FOR SEQ ID NO:351:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 144 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

Val Trp Leu Arg Gly Glu Leu Ala Glu Asp Ser Gly Glu Leu Pro Cys  
1 5 10 15  
Arg Arg Arg Gly Pro Gly Trp His Gly Phe Cys Ser Asp Ala Gly Pro  
20 25 30  
Arg Pro Ile Pro Leu Val Arg Pro Ala Ala Gly Tyr Pro Asp Pro Gly  
35 40 45  
Gly Ala Glu Arg Leu Leu Gln Leu Cys Pro Asp Leu His Gln Ser Gln  
50 55 60  
Ser His Leu Gln Pro Arg Leu Gln Gly Trp Glu Glu His Ala Ser Gln  
65 70 75 80  
Thr Leu Trp Gly Leu Ala Ala Glu Val Ser Gln Pro Val Ser Gly Phe  
85 90 95  
Ala Gly Glu Gln Pro Pro Asp Gly Val His Gln His Leu Gln Asp Pro  
100 105 110  
Pro Ala Ala Gly Val Gln Val Ser Arg Met Cys Ala Ala Ala Pro Ile  
115 120 125  
Ser Ser Ala Ser Leu Glu Glu Pro His Ile Phe Pro Ala Arg His Leu  
130 135 140

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

His Gly Leu Pro Leu Leu Leu His Pro Glu Ser Gln Glu Arg Arg Asp  
1 5 10 15  
Val Ala Gly Gly Gln Gly Arg Arg Arg Pro Ser Ala Leu Arg Gly Arg  
20 25 30  
Ala Val Ala Val Pro Pro Ser Ile Pro Ala Gln Ala Asp Ser Thr Pro  
35 40 45  
Cys His Leu Arg Ala Thr Pro Gly Val Thr Gln Asp Ser Pro Asp Ala  
50 55 60  
Ala Glu Ser Glu Ala Pro Gly Asp Asp Ala Asp Cys Pro Gly Gly Arg  
65 70 75 80  
Ser Gln Pro Gly Thr Ala Leu Arg Leu Gln Asp His Pro Gly Leu Met  
85 90 95

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Thr | Arg | Pro | Gln | Pro | Gly | Arg | Glu | Gln | Thr | Pro | Ala | Ala | Leu | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Arg | Ala | Leu | Arg | Pro | Arg | Glu | Gly | Gly | Ala | Ala | His | Thr | Gln | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Thr | Ala | Gly | Ser | Leu | Arg | Pro | Glu |     |     |     |     |     |     |     |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:353:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

|         |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val     | Phe | Gly | Arg | Gly | Leu | His | Val | Arg | Leu | Lys | Ala | Glu | Cys | Pro | Ala |
| 1       |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:354:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 71 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Val | Gln | Pro | Arg | Ala | Glu | Cys | Pro | Ala | His | Leu | Pro | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Pro | His | Arg | Leu | Ala | Leu | Gly | Ser | Thr | Pro | Gly | Pro | Ala | Phe | Pro |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| His | Gln | Glu | Pro | Gly | Phe | His | Ser | Pro | His | Arg | Asn | Ser | Pro | Ser | Pro |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Asp | Ser | Pro | Leu | Phe | Thr | Pro | Arg | Pro | Ala | Leu | Leu | Cys | Leu | Pro | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Pro | Pro | Ser | Arg | Trp | Arg | Pro |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:355:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 40 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Gly | Pro | Trp | Glu | Leu | Trp | Glu | Phe | Gly | Val | Thr | Lys | Gly | Val | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Thr | Gln | Ala | Arg | Thr | Leu | His | Leu | Asp | Gly | Gly | Pro | Cys | Gly | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Trp | Gly | Glu | Val | Leu | Trp | Glu |     |     |     |     |     |     |     |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:356:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Thr | Glu | Tyr | Met | Ser | Phe | Ser | Val | Leu | Lys | Lys | Lys | Lys | Lys | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:357:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 94 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ala | Ala | Ser | Cys | Cys | Ala | Arg | Gly | Lys | Pro | Trp | Pro | Arg | Pro | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Arg | Cys | Arg | Ala | Leu | Pro | Ala | Ala | Glu | Pro | Cys | Ala | Pro | Cys | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Ala Ala Thr Thr Ala Arg Cys Cys Arg Trp Pro Arg Ser Cys Gly Ala  
35 40 45

Trp Gly Pro Arg Ala Gly Gly Trp Cys Ser Ala Gly Thr Arg Arg Leu  
50 55 60

Ser Ala Arg Trp Trp Pro Xaa Ala Trp Cys Ala Cys Pro Gly Xaa Xaa  
65 70 75 80

Gly Xaa Pro Pro Pro Pro Pro Pro Ser Ala Arg Cys Pro Ala  
85 90

(2) INFORMATION FOR SEQ ID NO:358:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

Xaa Xaa Trp Trp Pro Glu Cys Cys Xaa Xaa Cys Ala Xaa Ala Ala Arg  
1 5 10 15

Xaa Thr Cys Trp Pro Ser Ala Ser Arg Cys Trp Thr Gly Pro Ala Gly  
20 25 30

Ala Pro Pro Arg Pro Ser Pro Pro Ala Cys Ala Ala Thr Cys Pro Thr  
35 40 45

Arg

(2) INFORMATION FOR SEQ ID NO:359:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1003 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

Pro Thr His Cys Gly Gly Ala Gly Arg Gly Gly Cys Cys Cys Ala Ala  
1 5 10 15

Trp Ala Thr Thr Cys Trp Phe Thr Cys Trp His Ala Ala Arg Xaa Leu  
20 25 30

Cys Trp Trp Xaa Pro Ala Ala Pro Thr Xaa Cys Ala Gly Arg Arg Cys  
35 40 45

Thr Ser Ser Ala Leu Xaa Leu Arg Pro Gly Pro Arg His Thr Leu Xaa  
 50 55 60  
 Asp Pro Xaa Ala Ser Gly Ile Gln Arg Ala Trp Asn His Ser Val Arg  
 65 70 75 80  
 Glu Ala Gly Val Pro Leu Gly Cys Gln Pro Arg Val Arg Gly Gly Ala  
 85 90 95  
 Gly Ala Val Pro Ala Glu Val Cys Arg Cys Pro Arg Gly Pro Gly Val  
 100 105 110  
 Ala Leu Pro Leu Ser Arg Ser Gly Arg Pro Leu Gly Arg Gly Pro Gly  
 115 120 125  
 Pro Thr Arg Ala Gly Arg Leu Asp Arg Val Thr Val Val Ser Val Trp  
 130 135 140  
 Cys His Leu Pro Asp Pro Pro Lys Lys Pro Pro Leu Trp Arg Val Arg  
 145 150 155 160  
 Ser Leu Ala Arg Ala Thr Pro Thr His Pro Trp Ala Ala Ser Thr Thr  
 165 170 175  
 Arg Ala Pro His Pro His Arg Gly His His Val Leu Gly His Ala Leu  
 180 185 190  
 Ser Pro Gly Val Arg Arg Asp Gln Ala Leu Pro Leu Leu Leu Arg Arg  
 195 200 205  
 Gln Xaa His Cys Xaa Pro Pro Ser Tyr Ser Ile Tyr Leu Arg Pro Ser  
 210 215 220  
 Leu Thr Gly Val Arg Glu Val Arg Gly Asp Xaa Leu Ser Gly Ser Arg  
 225 230 235 240  
 Pro Trp Met Pro Gly Phe Pro Ala Gly Cys Pro Ala Cys Pro Ser Xaa  
 245 250 255  
 Thr Gly Lys Cys Gly Pro Cys Phe Trp Ser Cys Leu Gly Thr Thr Arg  
 260 265 270  
 Ser Ala Pro Thr Gly Cys Ser Ser Arg Arg Thr Ala Arg Cys Glu Leu  
 275 280 285  
 Arg Ser Pro Gln Gln Pro Val Ser Val Pro Gly Arg Ser Pro Arg Ala  
 290 295 300  
 Leu Trp Arg Pro Pro Arg Arg Arg Asn Thr Asp Pro Arg Arg Leu Val  
 305 310 315 320  
 Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val  
 325 330 335  
 Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg  
 340 345 350  
 His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu  
 355 360 365

Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser  
 370 375 380  
 Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val  
 385 390 395 400  
 Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu  
 405 410 415  
 His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe  
 420 425 430  
 Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg  
 435 440 445  
 Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu  
 450 455 460  
 Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His  
 465 470 475 480  
 Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro  
 485 490 495  
 Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly  
 500 505 510  
 Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg  
 515 520 525  
 Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro  
 530 535 540  
 Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala  
 545 550 555 560  
 Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu  
 565 570 575  
 Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro  
 580 585 590  
 Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn  
 595 600 605  
 Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly  
 610 615 620  
 His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu  
 625 630 635 640  
 Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Xaa Asn Ser Pro  
 645 650 655  
 Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala  
 660 665 670  
 Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala  
 675 680 685

Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln  
690 695 700  
Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met  
705 710 715 720  
Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg  
725 730 735  
Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys  
740 745 750  
Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val  
755 760 765  
Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala  
770 775 780  
Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro  
785 790 795 800  
Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp  
805 810 815  
Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn  
820 825 830  
Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val  
835 840 845  
Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser  
850 855 860  
Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala  
865 870 875 880  
Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val  
885 890 895  
Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser  
900 905 910  
Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly  
915 920 925  
Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu  
930 935 940  
Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr  
945 950 955 960  
Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg  
965 970 975  
Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro  
980 985 990  
Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp  
995 1000

(2) INFORMATION FOR SEQ ID NO:360:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 38 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

```
Trp Pro Pro Ala His Ser Gln Ala Glu Ser Arg His Gln Gln Pro Cys
1 5 10 15

His Ala Gly Leu Tyr Val Pro Gly Arg Glu Gly Arg Pro Thr Pro Arg
 20 25 30

Pro Ala Pro Leu Gly Val
 35
```

(2) INFORMATION FOR SEQ ID NO:361:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 13 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

```
Gly Leu Ser Glu Cys Leu Ala Glu Ala Cys Met Ser Gly
1 5 10
```

(2) INFORMATION FOR SEQ ID NO:362:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 91 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

```
Arg Leu Ser Val Arg Leu Arg Pro Glu Arg Val Ser Ser Gln Gly Leu
1 5 10 15

Ser Val Gln His Thr Cys Arg Leu His Phe Pro Thr Gly Trp Arg Ser
 20 25 30

Ala Pro Pro Gln Gly Gln Leu Phe Leu Thr Arg Ser Pro Ala Ser Thr
 35 40 45
```

Pro His Ile Gly Ile Val His Pro Gln Ile Arg His Cys Ser Pro Leu  
50 55 60

Ala Leu Pro Ser Phe Ala Phe His Pro His His Pro Gly Gly Asp Pro  
65 70 75 80

Glu Lys Asp Pro Gly Ser Ser Gly Asn Leu Glu  
85 90

(2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

Pro Lys Val Cys Pro Val His Arg Arg Gly Pro Cys Thr Trp Met Gly  
1 5 10 15

Val Pro Val Gly Gln Ile Gly Gly Arg Cys Cys Gly Ser Lys Ile Leu  
20 25 30

Asn Ile

(2) INFORMATION FOR SEQ ID NO:364:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

Val Phe Gln Phe  
1

(2) INFORMATION FOR SEQ ID NO:365:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

Lys Lys Lys Lys Lys Lys Lys Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 1  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = polar amino acid,  
selected from Gly, Ser, Thr, Tyr, Cys,  
Asn or Gln"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

Xaa Phe Phe Tyr  
1

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 1  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 3  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

Xaa Arg Xaa Ile Pro Lys Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:368:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

Phe Arg Xaa Ile  
1

(2) INFORMATION FOR SEQ ID NO:369:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = charged amino acid,  
selected from Asp, Glu, His, Lys or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Pro Xaa Leu Tyr Phe Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Gly Ile Pro Gln Gly Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

Leu Leu Arg Leu  
1

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 5  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

Asp Asp Phe Leu Xaa Ile Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr  
1 5 10 15  
Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys  
20 25 30  
Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met Lys Met  
35 40 45

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Asn Asn Val Arg Met Asp Thr Gln Lys Thr Thr Leu Pro Pro Ala Val  
1 5 10 15  
Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg Leu Ile Thr Asn Leu  
20 25 30  
Arg Lys Arg Phe Leu Ile Lys Met Gly Ser Asn Lys Lys Met Leu Val  
35 40 45  
Ser Thr Asn Gln Thr Leu  
50

(2) INFORMATION FOR SEQ ID NO:375:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 34 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Phe Gly Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr  
1                  5                  10                  15  
Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys Lys Lys Leu  
                  20                  25                  30  
Lys Asp

(2) INFORMATION FOR SEQ ID NO:376:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 35 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser  
1                  5                  10                  15  
Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu  
                  20                  25                  30  
Ser Phe Thr  
                  35

(2) INFORMATION FOR SEQ ID NO:377:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 43 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys Lys  
1                  5                  10                  15

Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His  
                     20                    25                    30

Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile  
                     35                    40

(2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

Lys Lys Arg Met Pro Phe Phe Gly Phe Ser Val  
   1                    5                    10

(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr  
   1                    5                    10                    15

Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys  
                     20                    25                    30

Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys  
                     35                    40                    45

(2) INFORMATION FOR SEQ ID NO:380:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 54 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

[illegible]

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr  
1 5 10 15  
Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile  
20 25 30  
Lys Pro

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser  
1 5 10 15

Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe  
20 25 30

Ala Gly Ile  
35

(2) INFORMATION FOR SEQ ID NO:383:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 43 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

```
Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
1 5 10 15
His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
 20 25 30
Gly Cys Val Val Asn Leu Arg Lys Thr Val Val
 35 40
```

(2) INFORMATION FOR SEQ ID NO:384:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 11 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

```
His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu
1 5 10
```

(2) INFORMATION FOR SEQ ID NO:385:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 48 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

```
Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
1 5 10 15
Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
 20 25 30
Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp Leu Lys Lys
 35 40 45
```

(2) INFORMATION FOR SEQ ID NO:386:

- (i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 54 amino acids  
  (B) TYPE: amino acid  
  (C) STRANDEDNESS:  
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

```
Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys
1 5 10 15
Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe
20 25 30
Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr
35 40 45
Asn Thr Lys Leu Leu Asn
50
```

(2) INFORMATION FOR SEQ ID NO:387:

- (i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 34 amino acids  
  (B) TYPE: amino acid  
  (C) STRANDEDNESS:  
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

```
Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
1 5 10 15
Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
20 25 30
Leu Leu
```

(2) INFORMATION FOR SEQ ID NO:388:

- (i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 35 amino acids  
  (B) TYPE: amino acid  
  (C) STRANDEDNESS:  
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser  
1                   5                   10                   15  
Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu  
                  20                   25                   30  
Gly Phe Leu  
              35

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 43 amino acids  
  (B) TYPE: amino acid  
  (C) STRANDEDNESS:  
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln Glu Asn  
1                   5                   10                   15  
Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg Glu Asn  
                  20                   25                   30  
Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr  
              35                   40

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 11 amino acids  
  (B) TYPE: amino acid  
  (C) STRANDEDNESS:  
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

Gln Asp Tyr Cys Asp Trp Ile Gly Ile Ser Ile  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 47 amino acids  
  (B) TYPE: amino acid  
  (C) STRANDEDNESS:  
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Trp | Leu | Phe | Arg | Gln | Leu | Ile | Pro | Lys | Ile | Ile | Gln | Thr | Phe | Phe | Tyr |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Cys | Thr | Glu | Ile | Ser | Ser | Thr | Val | Thr | Ile | Val | Tyr | Phe | Arg | His | Asp |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Thr | Trp | Asn | Lys | Leu | Ile | Thr | Pro | Phe | Ile | Val | Glu | Tyr | Phe | Lys |     |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Cys | Arg | Asn | His | Asn | Ser | Tyr | Thr | Leu | Ser | Asn | Phe | Asn | His | Ser | Lys |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Met | Arg | Ile | Ile | Pro | Lys | Lys | Ser | Asn | Asn |     |     |     |     |     |     |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Phe | Arg | Ile | Ile | Ala | Ile | Pro | Cys | Arg | Gly | Ala | Asp | Glu | Glu | Glu | Phe |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Thr | Ile | Tyr | Lys | Glu | Asn | His | Lys | Asn | Ala | Ile | Gln | Pro |     |     |     |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

```
Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln Gln
1 5 10 15
Gln Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr
 20 25 30
Asn Ala Lys Ala Asn Arg Asp Lys Ile Leu Ala
 35 40
```

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

```
Lys Glu Leu Glu Val Trp Lys His Ser Ser Thr
1 5 10
```

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

```
Leu Ser Asn Glu Leu Gly Thr Gly Lys Phe Lys Phe Lys Pro Met Arg
1 5 10 15
Ile Val Asn Ile Pro Lys Pro Lys Gly Gly Ile Arg Pro Leu Ser Val
 20 25 30
Gly Asn Pro Arg Asp Lys Ile Val Gln Glu Val Met Arg Met Ile Leu
 35 40 45
Asp Thr Ile Phe Asp Lys Lys
 50 55
```

(2) INFORMATION FOR SEQ ID NO:397:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 34 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

```
Phe Gly Gly Ser Asn Trp Phe Ile Glu Val Asp Leu Lys Lys Cys Phe
1 5 10 15
Asp Thr Ile Ser His Asp Leu Ile Ile Lys Glu Leu Lys Arg Tyr Ile
 20 25 30
Ser Asp
```

(2) INFORMATION FOR SEQ ID NO:398:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 35 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

```
Thr Tyr His Lys Pro Met Leu Gly Leu Pro Gln Gly Ser Leu Ile Ser
1 5 10 15
Pro Ile Leu Cys Asn Ile Val Met Thr Leu Val Asp Asn Trp Leu Glu
 20 25 30
Asp Tyr Ile
 35
```

(2) INFORMATION FOR SEQ ID NO:399:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

```
Lys Met Ile Lys Arg Asp Leu Asn Asn Phe Leu Asn Ser Leu Gly Leu
1 5 10 15
```

Thr Ile Asn Glu Glu Lys Thr Leu Ile  
 20 25

(2) INFORMATION FOR SEQ ID NO:400:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

Arg Cys Val Val Glu Gly Thr Phe Pro Pro Val Trp Lys Asp Gly Arg  
 1 5 10 15  
 Leu Leu Val Leu Pro Lys Gly Asn Gly Arg  
 20 25

(2) INFORMATION FOR SEQ ID NO:401:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Tyr Arg Pro Val Thr Leu Leu Pro Val Leu Gly Lys Ile Leu Glu Lys  
 1 5 10 15  
 Val Leu Leu Gln Cys Ala Pro Gly Leu Thr His Ser Ile  
 20 25

(2) INFORMATION FOR SEQ ID NO:402:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Glu Gln Arg Tyr Val Met Ala Ile Phe Leu Asp Ile Ser Gly Ala Phe  
 1 5 10 15

Asp Asn Ala Trp Trp Pro Met Ile Met Val Lys Ala Lys Arg Asn Cys  
 20 25 30

Pro Pro

(2) INFORMATION FOR SEQ ID NO:403:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

Glu Trp Lys Val Ser Thr Met Gly Cys Pro Gln Gly Ser Val Leu Gly  
 1 5 10 15  
 Pro Thr Leu Trp Asn Val Leu Met Asp Asp Leu Leu Ala Leu Pro Gln  
 20 25 30  
 Gly Ile Glu  
 35

(2) INFORMATION FOR SEQ ID NO:404:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

Met Val Ala Tyr Ala Asp Asp Val Thr Val Leu Val Arg Gly Asp Ser  
 1 5 10 15  
 Arg

(2) INFORMATION FOR SEQ ID NO:405:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

Ala His Ala Val Leu Gly Leu Ala Glu Gly Trp Ala Ser Arg Asn Lys  
1 5 10 15  
Leu Asp Phe Ala Pro Ala Lys Ser Arg Cys  
20 25

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

Glu Asn Gln Val Thr Val Leu Gly Val Ser Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro  
1 5 10 15  
Val Phe Ala Ile Lys Lys Lys Asp Ser Thr  
20 25

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp  
1 5 10 15

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Trp | Glu | Val | Gln | Leu | Gly | Ile | Pro | His | Pro | Ala | Gly | Leu | Lys | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Lys | Ser | Val | Thr | Val | Leu | Asp | Val | Gly | Asp | Ala | Tyr | Phe | Ser | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Leu | Asp | Glu | Asp | Phe | Arg | Lys | Tyr | Thr | Ala | Phe | Thr | Ile | Pro |     |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:409:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ile | Arg | Tyr | Gln | Tyr | Asn | Val | Leu | Pro | Gln | Gly | Trp | Lys | Gly | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ala | Ile | Phe | Gln | Ser | Ser | Met | Thr | Lys | Ile | Leu | Glu | Pro | Phe | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Gln | Asn |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 35  |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:410:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Tyr | Gln | Tyr | Met | Asp | Asp | Leu | Tyr | Val | Gly | Ser | Asp | Leu | Glu | Ile |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:411:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Arg | Thr | Lys | Ile | Glu | Glu | Leu | Arg | Gln | His | Leu | Leu | Arg | Trp | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Thr | Thr | Pro | Asp | Lys | Lys | His | Gln | Lys | Glu | Pro | Pro | Phe | Leu | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Gly | Ile | Thr | Leu |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 35  |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Val | Val | Glu | Leu | Leu | Arg | Ser | Phe | Phe | Tyr | Val | Thr | Glu | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Phe | Gln | Lys | Asn | Arg | Leu | Phe | Phe | Tyr | Arg | Lys | Ser | Val | Trp | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Leu | Gln | Ser | Ile | Gly | Ile | Arg | Gln | His | Leu | Lys | Arg | Val | Gln | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Glu | Leu | Ser | Glu | Ala | Glu | Val | Arg | Gln | His | Arg | Glu | Ala | Arg | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Leu | Leu | Thr | Ser | Arg | Leu | Arg | Phe | Ile | Pro | Lys | Pro | Asp | Gly | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Pro | Ile | Val | Asn | Met | Asp | Tyr | Val | Val | Gly | Ala | Arg | Thr | Phe | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Glu | Lys | Arg | Ala | Glu | Arg | Leu | Thr | Ser | Arg | Val | Lys | Ala | Leu | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Val | Leu | Asn | Tyr | Glu | Arg | Ala | Arg | Arg | Pro | Gly | Leu | Leu | Gly | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Val | Leu | Gly | Leu | Asp | Asp | Ile | His | Arg | Ala | Trp | Arg | Thr | Phe | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Arg | Val | Arg | Ala | Gln | Asp | Pro | Pro | Pro | Glu | Leu | Tyr | Phe | Val | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Asp | Val | Thr | Gly | Ala | Tyr | Asp | Thr | Ile | Pro | Gln | Asp | Arg | Leu | Thr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Val | Ile | Ala | Ser | Ile | Ile | Lys | Pro | Gln | Asn | Thr | Tyr | Cys | Val | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala  
 195 200 205  
 Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg  
 210 215 220  
 Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val  
 225 230 235 240  
 Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe  
 245 250 255  
 Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly  
 260 265 270  
 Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser  
 275 280 285  
 Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe  
 290 295 300  
 Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe  
 305 310 315 320  
 Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr  
 325 330 335  
 Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys  
 340 345 350  
 Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala  
 355 360 365  
 Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu  
 370 375 380  
 Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala  
 385 390 395 400  
 Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala  
 405 410 415  
 Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys  
 420 425 430  
 His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys  
 435 440 445  
 Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala  
 450 455 460  
 Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr  
 465 470 475 480  
 Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile  
 485 490 495  
 Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala  
 500 505 510

Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe  
515 520 525

Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly  
530 535 540

Ser  
545

(2) INFORMATION FOR SEQ ID NO:413:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 79 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

Ser Gln His Xaa Gln Thr Leu Leu Ala Ala Met Pro Ile Ser Arg Leu  
1 5 10 15

Arg Phe Ile Pro Lys Pro Asn Trp Arg Pro Ile Val Asn Met Ser Tyr  
20 25 30

Ser Met Gly Ala Arg Ala Leu Gly Arg Arg Lys Gln Ala Gln His Phe  
35 40 45

Thr Gln Arg Leu Lys Thr Leu Phe Ser Met Leu Asn Tyr Glu Pro Glu  
50 55 60

Pro Asp Ile Lys Leu Ile Asp Thr Ala Gln Ser Thr Ser Arg Gly  
65 70 75

(2) INFORMATION FOR SEQ ID NO:414:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Ser Arg Leu Arg Phe Ile Pro Lys Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:415:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 6 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

Arg Pro Ile Val Asn Met  
1                    5

(2) INFORMATION FOR SEQ ID NO:416:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 4 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

Leu Asn Tyr Glu  
1

(2) INFORMATION FOR SEQ ID NO:417:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 535 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| AGAGCACCGT CTGCGTGAGG AGATCCTGGC CAAGTTCCTG CACTGGCTGA TGAGTGTGTA  | 60  |
| CGTCGTCGAG CTGCTCAGGT CTTTCTTTTA TGTCACGGAG ACCACGTTTC AAAAGAACAG  | 120 |
| GCTCTTTTTC TACCGGAAGA GTGTCTGGAG CAAGTTGCAA AGCATTGGAA TCAGACAGCA  | 180 |
| CTTGAAGAGG GTGCAGCTGC GGGAGCTGTC GGAAGCAGAG GTCAGGCAGC ATCGGGAAGC  | 240 |
| CAGGCCCGCC CTGCTGACGT CCAGACTCCG CTTTCATCCCC AAGCCTGACG GGCTGCGGCC | 300 |
| GATTGTGAAC ATGGACTACG TCGTGGGAGC CAGAACGTTT CGCAGAGAAA AGAGGGCCGA  | 360 |
| GCGTCTCACC TCGAGGGTGA AGGCACTGTT CAGCGTGCTC AACTACGAGC GGGCGCGGCG  | 420 |

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CCCCGGCCTC CTGGGCGCCT CTGTGCTGGG CCTGGACGAT ATCCACAGGG CCTGGCGCAC | 480 |
| CTTCGTGCTG CGTGTGCGGG CCCAGGACCC GCCGCCTGAG CTGTACTTTG TCAAG      | 535 |

(2) INFORMATION FOR SEQ ID NO:418:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 550 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| AGAGCACCGT CTGCGTGAGG AGATCCTGGC CAAGTTCCTG CACTGGCTGA TGAGTGTGTA  | 60  |
| CGTCGTCGAG CTGCTCAGGT CTTTCTTTTA TGTCACGGAG ACCACGTTTC AAAAGAACAG  | 120 |
| GCTCTTTTTC TACCGGAAGA GTGTCTGGAG CAAGTTGCAA AGCATTGGAA TCAGACAGCA  | 180 |
| CTTGAAGAGG GTGCAGCTGC GGGAGCTGTC GGAAGCAGAG GTSAGKCAGC ATCNRSARRC  | 240 |
| MMKGCTAGCM GCCMTGCYNA YSTCSAGACT SCGCTTCATC CCCAAGCCYR ACKGGCTGCG  | 300 |
| GCCSATTTGTG AACATGRRYT AYRKCRTGGG WGCCAGARCK TTSSGCAGAR RRAAGMRGGC | 360 |
| CCAGCATTTTC RCCSAGCGTC TCACCTCGAG GGTGAAGRCW CTSTTCAGCR TGCTCAACTA | 420 |
| YGAGCSGGCG CGGCRMYYCG RYMTCMWGGG CGCCTCTRTG CTGGGCCTGG ACGATATCCA  | 480 |
| CAGGGCCTGG CGCACCTTCG TGCTGCGTGT GCGGGCYCAG RRCMCGYCGM SKGRGSTGTA  | 540 |
| CTTTGTCAAG                                                         | 550 |

(2) INFORMATION FOR SEQ ID NO:419:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 239 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GAGTCAGCAT CNACAGACAC TGCTAGCAGC CATGCCNATC TCGAGACTGC GCTTCATCCC | 60  |
| CAAGCCCAAC TGGCGGCCCA TTGTGAACAT GAGTTATAGC ATGGGTGCCA GAGCTTTGGG | 120 |
| CAGAAGGAAG CAGGCCCAGC ATTTACCCA GCGTCTCAAG ACTCTCTTCA GCATGCTCAA  | 180 |
| CTATGAGCCG GAATTCGATA TCAAGCTTAT CGATACCGCT CAGAGCACGT CGAGGGGGG  | 239 |

(2) INFORMATION FOR SEQ ID NO:420:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

```
Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr
1 5 10 15

Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys
 20 25 30

Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile
 35 40
```

(2) INFORMATION FOR SEQ ID NO:421:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

```
Glu Ala Glu Val Arg
1 5
```

(2) INFORMATION FOR SEQ ID NO:422:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

```
Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val
1 5 10 15
```

(2) INFORMATION FOR SEQ ID NO:423:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr  
1                  5                  10                  15  
  
Ile

(2) INFORMATION FOR SEQ ID NO:424:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu  
1                  5                  10                  15  
  
Leu Cys Ser Leu Cys Tyr  
                  20

(2) INFORMATION FOR SEQ ID NO:425:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr  
1                  5                  10

(2) INFORMATION FOR SEQ ID NO:426:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Val | Pro | Glu | Tyr | Gly | Cys | Val | Val | Asn | Leu | Arg | Lys | Thr | Val | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

(2) INFORMATION FOR SEQ ID NO:427:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 11 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Cys | Gly | Leu | Leu | Leu | Asp | Thr | Arg | Thr | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

(2) INFORMATION FOR SEQ ID NO:428:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 43 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Leu | Tyr | Asn | Ser | Phe | Ile | Ile | Pro | Ile | Leu | Gln | Ser | Phe | Phe | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Thr | Glu | Ser | Ser | Asp | Leu | Arg | Asn | Arg | Thr | Val | Tyr | Phe | Arg | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Trp | Lys | Leu | Leu | Cys | Arg | Pro | Phe | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:429:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

Glu Asn Asn Val Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:430:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

Ala Val Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg Leu Ile Thr  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:431:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg  
1 5 10 15  
  
Ile

(2) INFORMATION FOR SEQ ID NO:432:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser Ser Phe  
1 5 10 15  
Leu Cys His Phe Tyr Met  
20

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Gly Phe Glu Lys His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:436:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ile | Phe | Glu | Asp | Leu | Val | Val | Ser | Leu | Ile | Arg | Cys | Phe | Phe | Tyr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Thr | Glu | Gln | Gln | Lys | Ser | Tyr | Ser | Lys | Thr | Tyr | Tyr | Tyr | Arg | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ile | Trp | Asp | Val | Ile | Met | Lys | Met | Ser | Ile |     |     |     |     |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:437:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Glu | Lys | Glu | Val | Glu |
| 1   |     |     |     | 5   |

(2) INFORMATION FOR SEQ ID NO:438:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Lys | Leu | Arg | Leu | Ile | Pro | Lys | Lys | Thr | Thr | Phe | Arg | Pro | Ile | Met |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

(2) INFORMATION FOR SEQ ID NO:439:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser  
1                      5                      10                      15  
Val

(2) INFORMATION FOR SEQ ID NO:440:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile  
1                      5                      10                      15  
Leu Ser Ser Phe Tyr Tyr  
20

(2) INFORMATION FOR SEQ ID NO:441:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO:442:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Arg | Glu | Asn | Gly | Phe | Lys | Phe | Asn | Met | Lys | Lys | Leu | Gln | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

(2) INFORMATION FOR SEQ ID NO:443:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ile | Gly | Ile | Ser | Ile | Asp | Met | Lys | Thr | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

(2) INFORMATION FOR SEQ ID NO:444:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Leu | Phe | Arg | Gln | Leu | Ile | Pro | Lys | Ile | Ile | Gln | Thr | Phe | Phe | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Thr | Glu | Ile | Ser | Ser | Thr | Val | Thr | Ile | Val | Tyr | Phe | Arg | His | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Trp | Asn | Lys | Leu | Ile | Thr | Pro | Phe | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |

(2) INFORMATION FOR SEQ ID NO:445:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

Glu Asn Asn Val Cys  
1 5

(2) INFORMATION FOR SEQ ID NO:446:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn  
1 5 10

(2) INFORMATION FOR SEQ ID NO:447:

- (i) SEQUENCE CHARACTERISTICS:-
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

Phe Arg Ile Ile Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:448:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser  
1                      5                      10                      15  
  
Ile

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro  
1                      5                      10                      15  
  
Ile Val Asp Leu Val Tyr  
                    20

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 13 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys Ile Leu Ala  
1                      5                      10                      15

(2) INFORMATION FOR SEQ ID NO:452:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Lys | His | Ser | Ser | Thr | Met | Asn | Asn | Phe | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

(2) INFORMATION FOR SEQ ID NO:453:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

|     |     |     |     |
|-----|-----|-----|-----|
| Ile | Pro | Lys | Lys |
| 1   |     |     |     |

(2) INFORMATION FOR SEQ ID NO:454:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Leu | Leu | Leu | Arg | Leu |
| 1   |     |     | 5   |     |

(2) INFORMATION FOR SEQ ID NO:455:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

Asp Asp Phe Leu  
1

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

GGYTTNGGDA TRAANC

16

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

GCNTAYGAYA CNAT

14

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

TANGTRTCRT ANG

14

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:  
GGNATHCCNC ARGG 14

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:  
SWNCCYTGNNG GDATNCC 17

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:  
YTNGTNGAYG AYTTYYT 17

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:  
GTNACNARNA RRAARTCRTC 20

(2) INFORMATION FOR SEQ ID NO:463:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

Asp Asp Phe Leu Leu Val Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:464:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met, or Tyr"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 13  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = hydrophobic amino acid,  
                                       selected from Ala, Leu, Ile, Val, Pro,  
                                       Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Xaa | Xaa | Asp | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| 1   |     |     |     | 5   |     |     |     |     |     |     |     | 10  |

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 1  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = hydrophobic amino acid,  
                                       selected from Ala, Leu, Ile, Val, Pro,  
                                       Phe, Trp or Met, or Gln, Arg or Gly"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Gln | Gly | Xaa | Xaa | Xaa | Ser | Xaa |
| 1   |     |     |     | 5   |     |     |     |     |     |     |     | 10  |

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 1  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = hydrophobic amino acid,  
                                       selected from Ala, Leu, Ile, Val, Pro,  
                                       Phe, Trp or Met, or His or Tyr"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 5  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid,  
 selected from Ala, Leu, Ile, Val, Pro,  
 Phe, Trp or Met, or Thr"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 8  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid,  
 selected from Ala, Leu, Ile, Val, Pro,  
 Phe, Trp or Met, or Tyr"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 9  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid,  
 selected from Ala, Leu, Ile, Val, Pro,  
 Phe, Trp or Met, or Tyr or Lys"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 10  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid,  
 selected from Ala, Leu, Ile, Val, Pro,  
 Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Xaa | Xaa | Xaa | Asp | Asp | Xaa | Xaa | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 2  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid,  
 selected from Ala, Leu, Ile, Val, Pro,  
 Phe, Trp or Met, or Cys"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 4  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = hydrophobic amino acid,  
                                       selected from Ala, Leu, Ile, Val, Pro,  
                                       Phe, Trp or Met, or Lys or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

Gly Xaa Xaa Xaa Xaa Xaa Xaa Lys  
 1                              5

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 1  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = hydrophobic amino acid,  
                                       selected from Ala, Leu, Ile, Val, Pro,  
                                       Phe, Trp or Met, or Cys, Lys or Tyr"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 3  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = hydrophobic amino acid,  
                                       selected from Ala, Leu, Ile, Val, Pro,  
                                       Phe, Trp or Met, or Ser or Tyr"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 6  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = hydrophobic amino acid,  
                                       selected from Ala, Leu, Ile, Val, Pro,  
                                       Phe, Trp or Met, or Tyr"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 8  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = hydrophobic amino acid,  
                                       selected from Ala, Leu, Ile, Val, Pro,  
                                       Phe, Trp or Met, or Arg or Gln"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Thr, Lys, Tyr or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Glu, Lys or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Cys or Ala"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 10  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = hydrophobic amino acid,  
                                       selected from Ala, Leu, Ile, Val, Pro,  
                                       Phe, Trp or Met, or Tyr"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 11  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = Asp or Phe"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 12  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = Ser or Thr"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 13  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = hydrophobic amino acid,  
                                       selected from Ala, Leu, Ile, Val, Pro,  
                                       Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Xaa | Xaa | Asp | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| 1   |     |     |     | 5   |     |     |     |     |     |     |     | 10  |

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 3  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = Thr or Lys"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 4  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = Met, Phe or Val"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 6  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = Ile or Val"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 7  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = Glu or Lys"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 9  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = Cys or Ala"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 12  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = Ser or Thr"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 13  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = Ile or Val"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Xaa | Xaa | Xaa | Asp | Xaa | Xaa | Xaa | Xaa | Tyr | Asp | Xaa | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 48 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 2  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = Leu or Ile"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 7  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = hydrophobic amino acid,  
                                       selected from Ala, Leu, Ile, Val, Pro,  
                                       Phe, Trp or Met"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 8  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = hydrophobic amino acid,  
                                       selected from Ala, Leu, Ile, Val, Pro,  
                                       Phe, Trp or Met"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 10  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = hydrophobic amino acid,  
                                       selected from Ala, Leu, Ile, Val, Pro,  
                                       Phe, Trp or Met"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 11  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = hydrophobic amino acid,  
                                       selected from Ala, Leu, Ile, Val, Pro,  
                                       Phe, Trp or Met"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 12  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = Gln or Arg"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 29  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = Phe or Tyr"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 30  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = Phe or Tyr"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 38  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = Leu or Ile"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 41  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = hydrophobic amino acid,  
                                       selected from Ala, Leu, Ile, Val, Pro,  
                                       Phe, Trp or Met"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 48  
 (D) OTHER INFORMATION: /product= "OTHER"  
                               /note= "Xaa = Lys or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

```
Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
1 5 10 15
Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa
20 25 30
Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Xaa Xaa Xaa Xaa Xaa
35 40 45
```

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

```
Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Ile Pro Lys Lys
1 5 10
```

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

Xaa Arg Xaa Xaa Pro Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Phe or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

Xaa Arg Xaa Ile Xaa Xaa Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 6  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 8  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 10  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

Pro Xaa Leu Tyr Phe Xaa Xaa Xaa Asp Xaa Xaa Xaa Cys Tyr Asp Xaa  
1 5 10 15  
Ile

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

Leu Leu Arg Leu Xaa Asp Asp Xaa Leu Xaa Ile Thr  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO:477:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

Arg Lys Xaa Xaa Trp Xaa Xaa Leu  
1                      5

(2) INFORMATION FOR SEQ ID NO:478:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"



(i) SEQUENCE DESCRIPTION: SEQ ID NO:478:

Xaa Arg Xaa Xaa Pro Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

Leu Leu Leu Arg Leu Xaa Asp Asp Phe Leu  
1 5 10